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FIG. 1

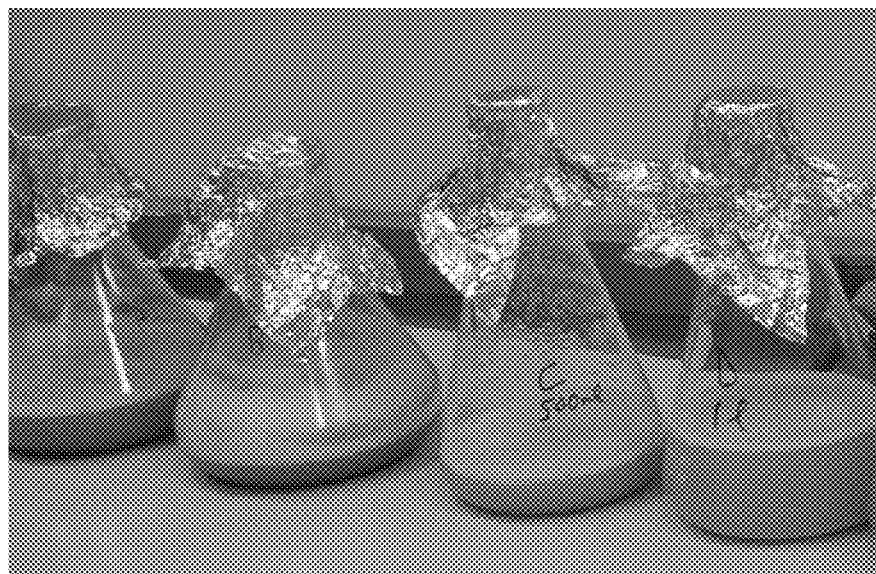


FIG. 2

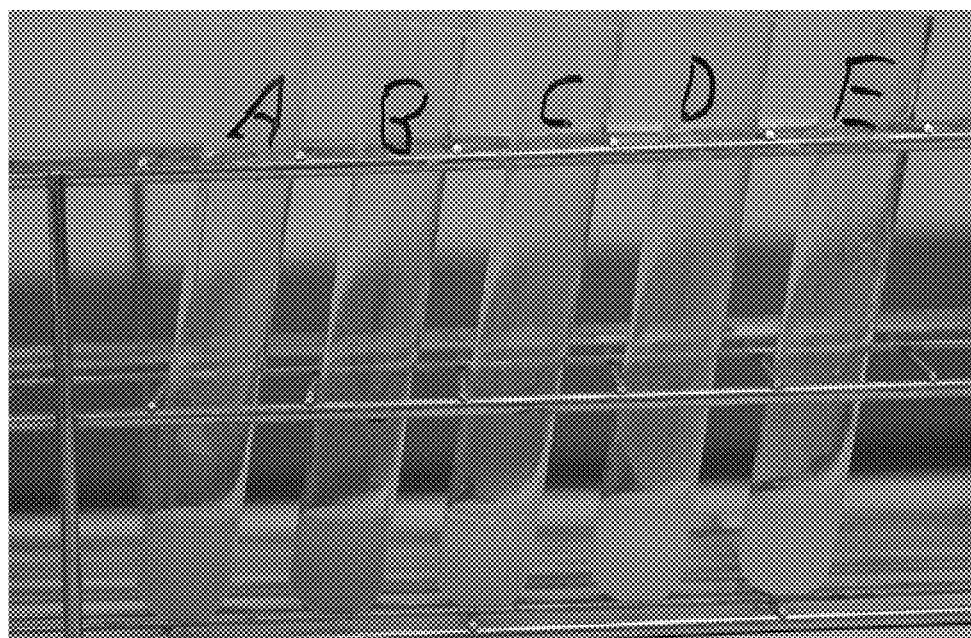


FIG. 3

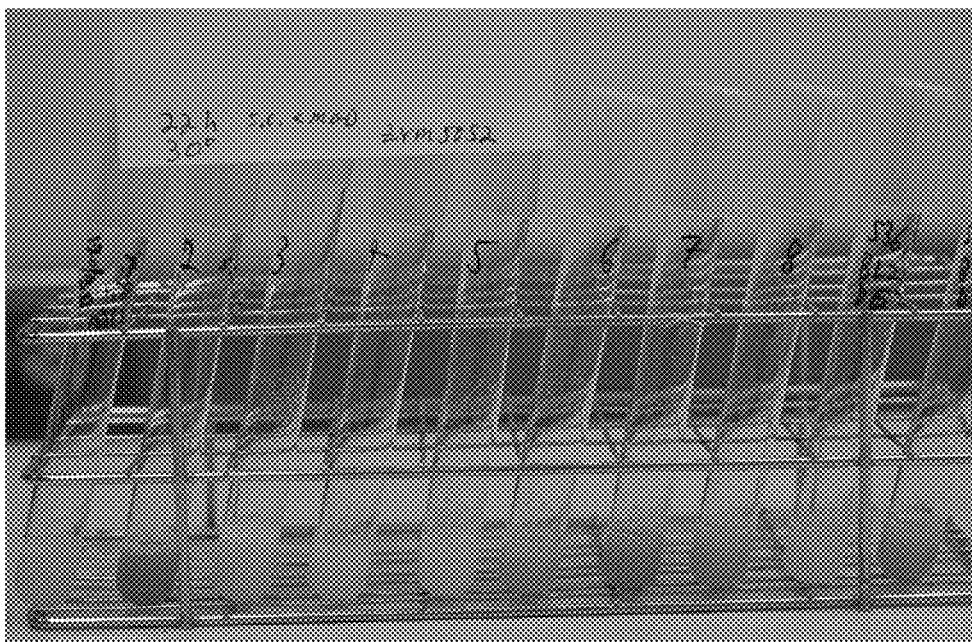
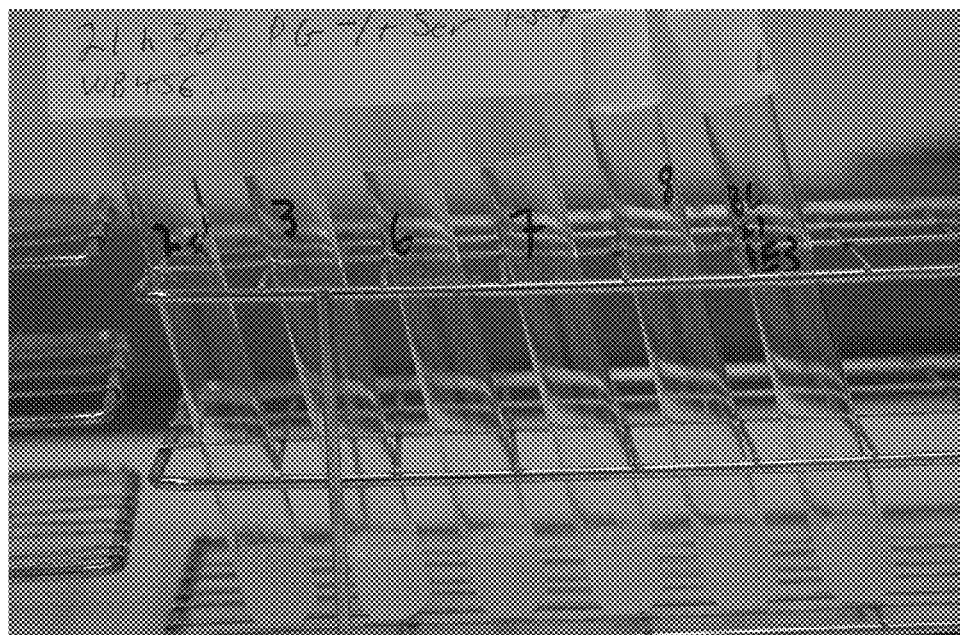


FIG. 4

A



B

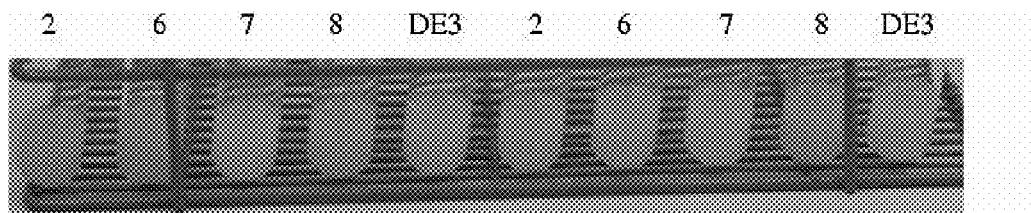


FIG. 5



FIG. 6

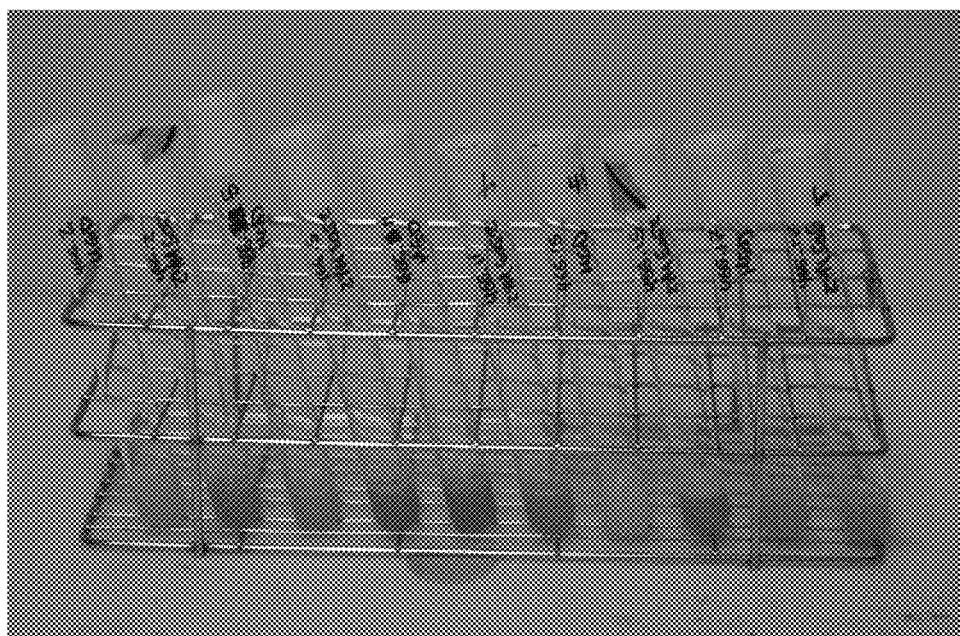


FIG. 7

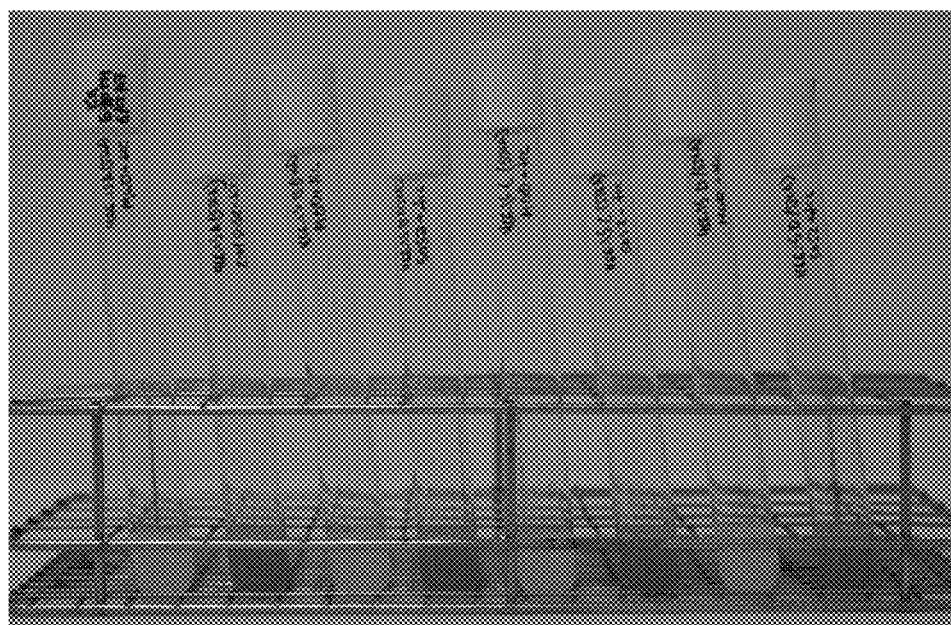


FIG. 8

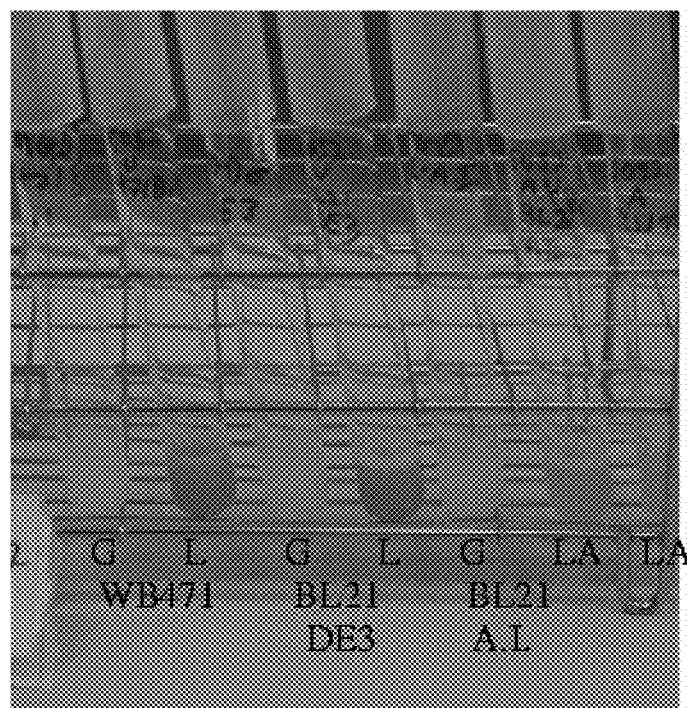


FIG. 9

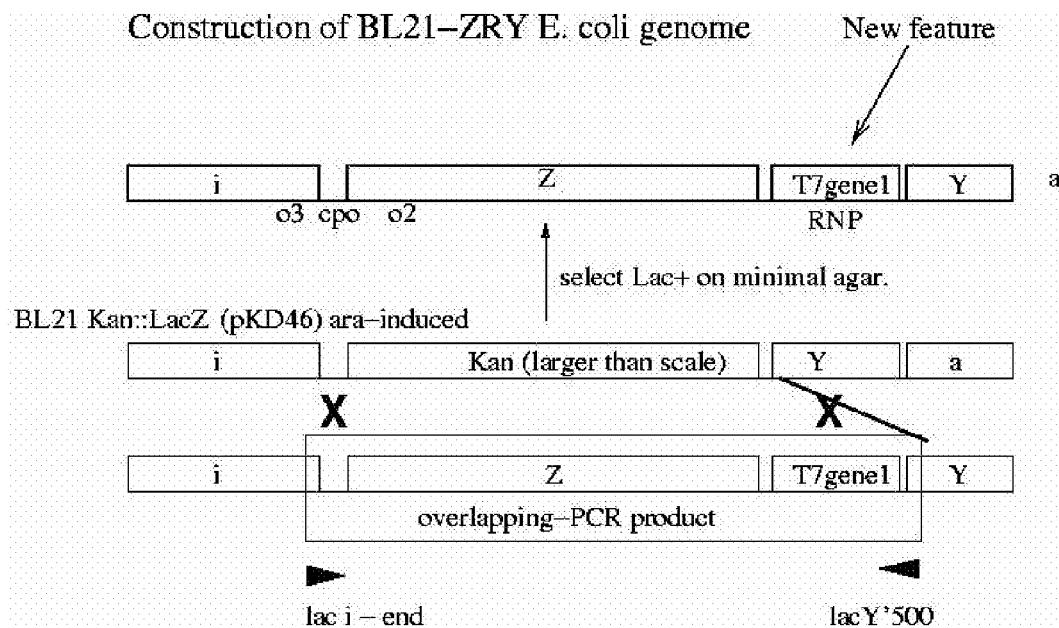


FIG. 10

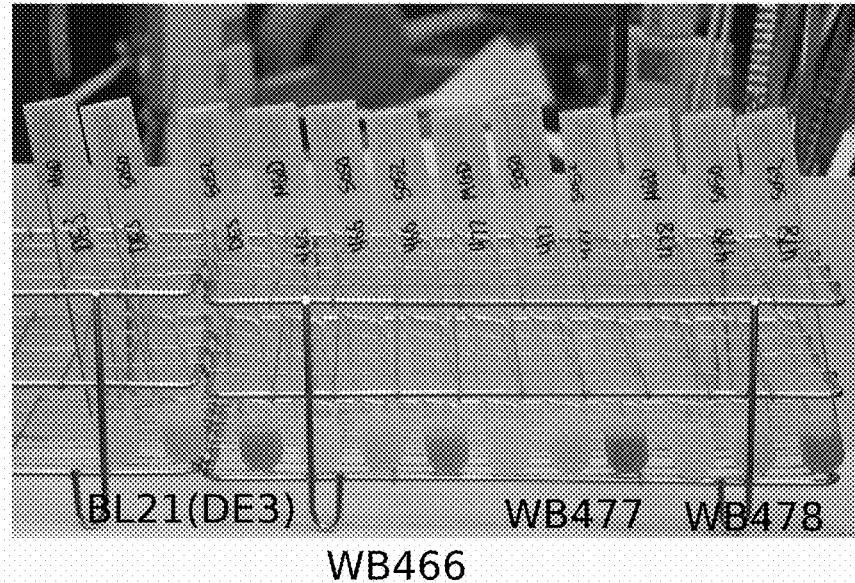
3240 3250 3260 3270 3280
TGGTGTCAAAAATAACTGGAAGAGGCACAAATGAACACGATT
TrpCysGlnLys*** MetAsnThrIle
Lac Z T7 RNA Polymerase (2.5 kb)

.....

5910 5920 5930 5940 5950
TTCGCGTTCGCGTAAGGAAATCCATTATGTAATTTAAAAAAC
PheAlaPheAla*** MetTyrTyrLeuLysAsn
T7 RNA polymerase Lac Y

..... indicates T7 phage DNA homology
----- indicates E. coli genome homology

FIG. 11



Red/Green Ratio (- gray BG of 1.09)

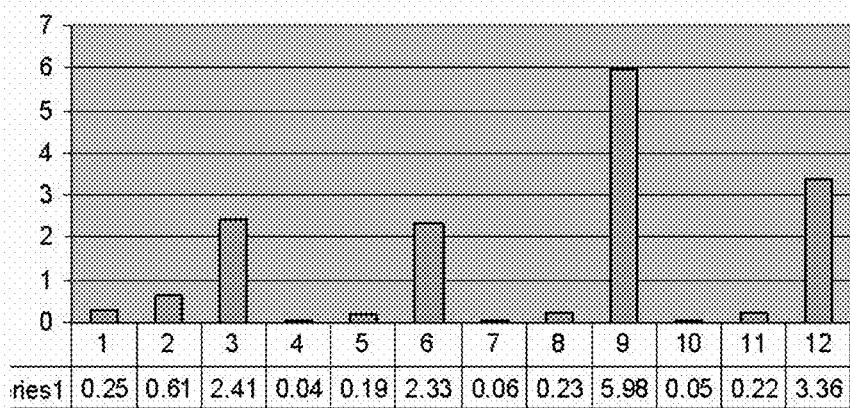
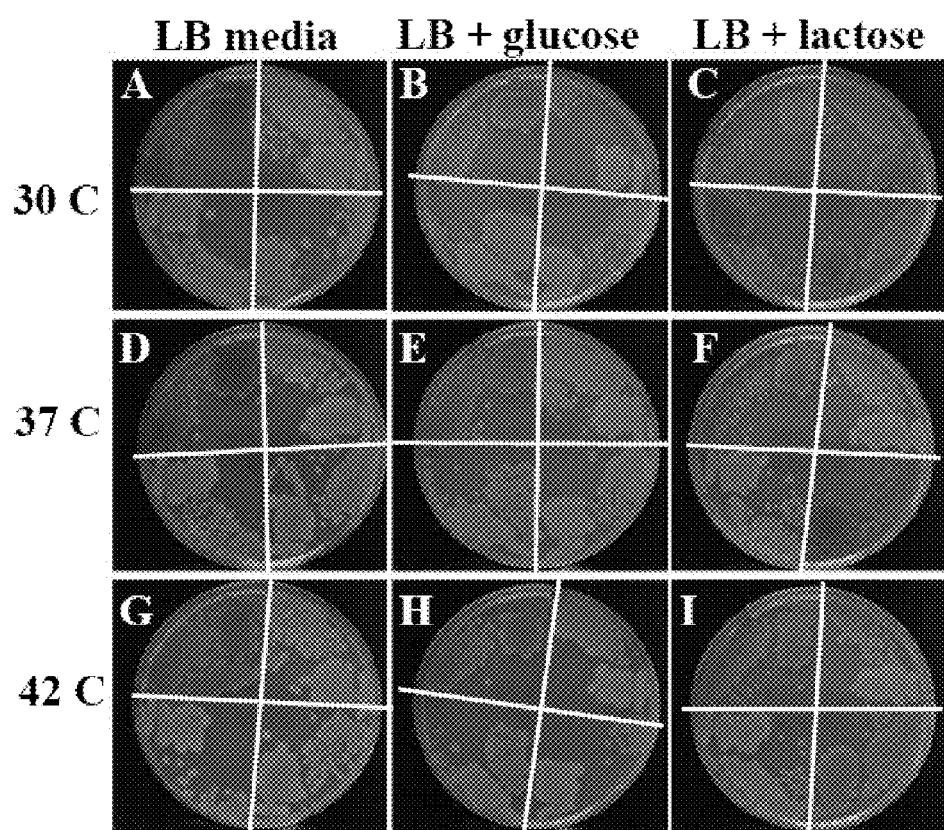


FIG. 12



1**T7 EXPRESSION SYSTEM****CROSS-REFERENCE TO RELATED APPLICATIONS**

This application is a national stage application under 35 U.S.C. §371 claiming priority to PCT/US2008/72644, filed Aug. 8, 2008, which in turn claims priority to U.S. Provisional Application Ser. No. 60/954,788, filed Aug. 8, 2007, each of which is incorporated herein by reference in its entirety.

INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED IN COMPUTER READABLE FORM

The Sequence Listing, which is a part of the present disclosure, includes a computer readable form comprising nucleotide and/or amino acid sequences of the present invention. The subject matter of the Sequence Listing is incorporated herein by reference in its entirety.

FIELD

The present invention generally relates to a system for expressing genes to proteins in *E. coli*.

BACKGROUND

T7 promoters have been used to achieve control of the expression of exogenous genes in *E. coli*, since their expression can be turned on by controlling the presence and expression of the T7 gene 1 (SEQ ID NO: 1) for T7 RNA polymerase (SEQ ID NO: 2) (Studier & Moffat, 1986; Studier et al., 1990; Tabor & Richardson, 1985). Phage T7 RNA polymerase does not recognize *E. coli* promoters, and vice versa (i.e., *E. coli* RNA polymerase does not recognize T7 promoters, except for the special “*E. coli*” one that transcribes gene 1).

The *E. coli* lac operon has been characterized (see e.g., Dickson et al, 1974; Schultz, Shields, & Steitz, 1991; Oehler, et al. 1990; Flashner & Gralla, 1988). The polycistronic lac operon mRNA molecule encodes three genes: Lac Z, Lac Y and Lac A. The product of the Lac Z coding region functions as a β -galactosidase; this function is required for the metabolism of lactose into glucose and galactose. The product of the Lac Y coding region functions as a lactose permease, which is a membrane-bound transport protein that allows lactose to enter the cell. Lac A is a β -galactosidase transacetylase, and does not appear to be strictly required for lactose metabolism.

The lactose operon genetic control region contains binding sites for 3 control proteins: CAP, RNA polymerase, and lac repressor (Dickson et al, 1974). Mutation L8 (a.k.a. L37) is a G to A transition (Dickson et al., 1977) in the CAP site, which eliminates the possibility of binding or activation by CAP protein when glucose is absent. Since binding by CAP protein activates the lac promoter 16-fold by introducing a 90° bend (Schultz, Shields, & Steitz, 1991), the L8 mutation results in a decreased level of transcription (e.g., to 6%). The phenotype is slightly Lac+ but melibiose negative at 42° C. (Ippen et al. 1968). During genetic analysis of the lac operon, second-site Lac+ (i.e., raffinose+) revertants of this CAP site mutant were selected after UV mutagenesis (Arditti et al, 1968; Silverstone et al. 1970), with the UV5 mutant consisting of a further change of two adjacent base pairs in the RNA polymerase binding site. The resulting promoter region, with a total of 3 base-pair changes, produced a promoter that is stronger than lac wild-type and oblivious to glucose repression, yet is still

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under control of lac repressor. The resultant L8-UV5 has been widely useful as a model promoter for basic transcription studies. As for the repressor, it is a tetrameric dimer-of-dimers and must bind at least two operators to achieve its full level of repression: Part of the binding of, and control by, the lac repressor depends on operator O2, some 400 bp into the lacZ gene (Oehler, et al. 1990; Flashner & Gralla, 1988). Operator O3, in the I gene, overlaps the CAP site so nearly that it has been proposed to ‘repress’ by interfering with CAP binding (Oehler et al, 1990); in parallel, it may serve to auto-repress the I gene.

Studier (2005) has recently formulated a mixture of sugars consisting of 0.5% glycerol, 0.05% glucose, and 0.2% lactose (ZYM-5052; herein “5052”) to replace the manual addition of inducer IPTG, achieving effective and convenient “auto-induction” of cultures for the purpose of exogenous protein production in *E. coli*. The host strain for this system is BL21 (DE3), a lysogen of phage lambda DE3 carrying the T7 gene 1 (SEQ ID NO: 1) under the control of the lac L8-UV5 promoter.

Auto-induction polypeptide expression systems rely on the principle that an inducer can induce production of target protein but is prevented from doing so by compounds that can be depleted during growth. This allows use of media in which target protein is produced automatically, without the need to monitor growth and add inducer at the proper time. Ideal auto-induction systems allow the host strain to grow in auto-inducing medium without expressing target protein until rather high density, when depletion of inhibitory factors would allow the inducer present in the medium to induce expression, thus producing high concentrations of target protein. For example, glucose in the medium can prevent the uptake and utilization of lactose inducer but when glucose is depleted, the lactose inducer can effectively induce expression of the target protein. Auto-induction is generally preferred over IPTG induction for increased simplicity (e.g., no need to follow culture growth or add inducer at the proper time), increased culture density, and increased concentration of target protein per volume of culture.

But, like all known inducible promoter systems, auto-induction polypeptide expression systems have a residual level of activity or “leakiness”, which leads to the inappropriate transcription and expression of the gene being cloned under the control of the promoter.

The auto-inducing expression system of Studier (2005) is widely used in the industry. Additionally, there exist several modifications to the system. For example, some researchers have inserted the T7 RNA polymerase (gene I) into lacZ (e.g., New England Biolabs), which is reported to provide better control but at the expense of auto-induction (because auto-induction requires lacZ (β -galactosidase) to make the inducer allolactose). As another example, some researchers have aligned T7 RNA polymerase gene I with the arabinose promoter (e.g., Invitrogen), but one must include arabinose in addition to 5052 sugar mixture for auto-induction. The inventor has observed that the auto-induced level is not as high with this strain, and it has a leaky background in Studier’s recommended non-inducing medium. As another example, strains have been selected as resistant to several families of toxic proteins (e.g., Miroux & Walker, 1996; Lucigen). As another example, the gene for T7 lysozyme, a natural inhibitor of T7 RNA polymerase, has been included on another (chloramphenicol-resistant) plasmid (Studier 1991). Further examples include plasmid copy-number control for the T7 expression vector (e.g., pETcoco, Novagen), and the addition of another lac operator (although it now has O1 and O3) to the pET vector series.

Thus there exists a need for improvements to the auto-induction expression system in which the T7 gene 1 is under control of the lac L8-UV5 promoter, especially with regard to reducing the uninduced leaky level of expression.

SUMMARY

The present invention provides an improved T7 expression system using, in part, the *E. coli* wild-type lac promoter-operator region, resulting in a tightly controlled host strain construct that can control uninduced, leaky expression of proteins while still auto-inducing well. The present teachings address and overcome the problem of promoter leakiness by providing a host strain that comprises a T7 polymerase gene inserted between lac Z and lac Y of the lac operon (a "ZRY strain"), downstream of an otherwise wild-type lac operon control region. Embodiments of the present invention to the host genome can be transparently compatible with, and additive to, various existing genomic and/or plasmid improvements.

One aspect of the invention provides an isolated ZRY construct. A first polynucleotide sequence (R) comprises one of: (a) an isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO: 2; (b) an isolated polynucleotide comprising SEQ ID NO: 1 encoding a T7 RNA polymerase; (c) an isolated polynucleotide comprising a nucleotide sequence which has at least 95% identity to that of SEQ ID NO: 1 over the entire length thereof and which encodes a polypeptide having RNA polymerase activity; (d) an isolated polynucleotide that hybridizes under stringent conditions to SEQ ID NO: 1 over the entire length of SEQ ID NO: 1; said stringent conditions comprising incubation at 65° C. in a solution comprising 6×SSC (0.9 M sodium chloride and 0.09 M sodium citrate); and which encodes a polypeptide having RNA polymerase activity; or (e) an isolated polynucleotide complementary to the polynucleotide sequence of (a), (b), (c), or (d). Z is a lac Z polynucleotide sequence encoding β-galactosidase. Y is a lac Y polynucleotide sequence encoding a β-galactoside permease. The isolated construct also comprises a wild-type lac control region (C) comprising a CAP binding site, a promoter, an operator, and a ribosome binding site. The polynucleotide encoding T7 RNA polymerase or mutant T7 RNA polymerase is located between lac Z and lac Y. ZRY is downstream of the wild-type lac control region. The promoter of the wild-type lac control region is a lac-inducible and catabolite-repressible promoter recognized by a host cell polymerase. And the polynucleotide encoding the T7 RNA polymerase or mutant T7 RNA polymerase is under the control of the lac-inducible and catabolite-repressible promoter.

Another aspect of the invention provides an expression system for producing a target polypeptide in a host cell. The expression system comprises an isolated DNA construct, as described above. The expression system also comprises a target promoter polynucleotide sequence recognized by the encoded T7 RNA polymerase of ZRY. The expression system also comprises a polynucleotide sequence encoding a target polypeptide. The polynucleotide sequence encoding a target target polypeptide is under control of the target promoter polynucleotide sequence.

Another aspect of the invention provides a transformed prokaryotic cell. The transformed prokaryotic cell comprises an isolated ZRY construct, as described above. Or the transformed prokaryotic cell comprises a ZRY expression system, as described above. Or the transformed prokaryotic cell comprises a polynucleotide sequence (R) encoding a T7 RNA polymerase or mutant T7 RNA polymerase selected from: (a)

a isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO: 2; (b) an isolated polynucleotide comprising SEQ ID NO: 1 encoding a T7 RNA polymerase; (c) an isolated polynucleotide comprising a nucleotide sequence which has at least 95% identity to that of SEQ ID NO: 1 over the entire length thereof and which encodes a polypeptide having RNA polymerase activity; (d) an isolated polynucleotide that hybridizes under stringent conditions to SEQ ID NO: 1 over the entire length of SEQ ID NO: 1; said stringent conditions comprising incubation at 65° C. in a solution comprising 6×SSC (0.9 M sodium chloride and 0.09 M sodium citrate); and which encodes a polypeptide having RNA polymerase activity; or (e) an isolated polynucleotide complementary to the polynucleotide sequence of (a), (b), (c), or (d). The polynucleotide encoding T7 RNA polymerase or mutant T7 RNA polymerase is located between lac Z and lac Y. ZRY is downstream of the wild-type lac control region. And the polynucleotide encoding the T7 RNA polymerase or mutant T7 RNA polymerase is under the control of the lac-inducible and catabolite-repressible promoter. In various embodiments, one of both of lac Z and lac Y can be endogenous to the host cell.

Another aspect of the invention provides a method for producing a target polypeptide in a host cell. The method comprises providing an isolated ZRY construct, as described above; or providing a polynucleotide sequence (R) encoding a T7 RNA polymerase or a mutant T7 RNA polymerase, as described above. The method also comprises providing a polynucleotide sequence encoding a target polypeptide under control of a target promoter polynucleotide sequence, which is recognized by the encoded T7 RNA polymerase or mutant T7 RNA polymerase. The method further comprises introducing the ZRY construct into the host cell, or introducing the polynucleotide sequence encoding the T7 RNA polymerase or mutant T7 RNA polymerase between lac Z and lac Y of the host cell, where ZRY is downstream of a wild-type lac control region; and the polynucleotide sequence (R) is under control of a lac-inducible and catabolite-repressible promoter of the wild-type lac control region. The method further comprises introducing into the host cell the polynucleotide sequence encoding the target polypeptide under control of the target promoter. The method further comprises incubating the host cell under conditions appropriate for expression of a T7 RNA polymerase encoded by the first polynucleotide sequence (R) and expression of the target polypeptide from the target polynucleotide sequence.

In various embodiments, the host cell further comprises a polynucleotide encoding a colorimetric positive indicator of T7 RNA polymerase expression. In some embodiments, the colorimetric positive indicator is DsRed.T3.

In various embodiments, the host cell is an *E. coli* cell. In some embodiments, the host cell is an *E. coli* strain selected from the group consisting BL21, C2566, DH1, DH4I, DH5, DH5I, DH5IF', DH5IMCR, DH10B, DH10B/p3, DH11S, C600, HB101, JM101, JM105, JM109, JM110, K38, MG1655, RR1, Y1088, Y1089, CSH18, ER1451, and ER1647. In some embodiments, the host cell is *E. coli* strain BL21.

In various embodiments, the transformed cell is *E. coli* strain WB456.7, *E. coli* strain WB466.15, *E. coli* strain WB478e, or *E. coli* strain WB477f.

In various embodiments, the first polynucleotide sequence (R) comprises an isolated nucleotide sequence having at least 95% identity to SEQ ID NO: 1 over the entire length thereof and encoding a polypeptide having T7 RNA polymerase activity.

In various embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that: has at least 95% identity to SEQ ID NO: 1 over the entire length thereof; has at least one mutation selected from the group consisting of: a mutation at base 251 of CGC to CAC; a mutation at base 1240 of ATC to GTC; a mutation at base 1958 of GAT to GGT; a mutation at base 2092 from TGG to GGG; and a mutation at base 2203 from GTG to ATG; and encodes a polypeptide having RNA polymerase activity. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 3; SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; and SEQ ID NO: 11. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NO: 4; SEQ ID NO: 6; SEQ ID NO: 8; SEQ ID NO: 10; and SEQ ID NO: 12.

In various embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that: has at least 95% identity to SEQ ID NO: 1 over the entire length thereof; has at least two mutations selected from the group consisting of: a mutation at base 251 of CGC to CAC; a mutation at base 1240 of ATC to GTC; a mutation at base 1958 of GAT to GGT; a mutation at base 2092 from TGG to GGG; and a mutation at base 2203 from GTG to ATG; and encodes a polypeptide having RNA polymerase activity. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; and SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; SEQ ID NO: 29; and SEQ ID NO: 31. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence of SEQ ID NO: 31. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24; SEQ ID NO: 26; SEQ ID NO: 28; SEQ ID NO: 30; and SEQ ID NO: 32. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that encodes an amino acid sequence of SEQ ID NO: 32.

In various embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that: has at least 95% identity to SEQ ID NO: 1 over the entire length thereof; has at least three mutations selected from the group consisting of: a mutation at base 251 of CGC to CAC; a mutation at base 1240 of ATC to GTC; a mutation at base 1958 of GAT to GGT; a mutation at base 2092 from TGG to GGG; and a mutation at base 2203 from GTG to ATG; and encodes a polypeptide having RNA polymerase activity. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 33; SEQ ID NO: 35; SEQ ID NO: 37; SEQ ID NO: 39; and SEQ ID NO: 41; SEQ ID NO: 43; SEQ ID NO: 45; SEQ ID NO: 47; SEQ ID NO: 49; and SEQ ID NO: 51. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence of SEQ ID NO: 49. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NO: 34; SEQ ID NO: 36; SEQ ID NO: 38; SEQ ID NO: 40; and SEQ ID NO: 42; SEQ ID NO: 44; SEQ ID NO: 46; SEQ ID NO: 48; SEQ ID NO: 50; and SEQ ID NO: 52. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that encodes an amino acid sequence of SEQ ID NO: 50.

In various embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that: has at least 95% identity to SEQ ID NO: 1 over the entire length thereof; has at least four mutations selected from the group consisting of: a mutation at base 251 of CGC to CAC; a mutation at base 1240 of ATC to GTC; a mutation at base 1958 of GAT to GGT; a mutation at base 2092 from TGG to GGG; and a mutation at base 2203 from GTG to ATG; and encodes a polypeptide having RNA polymerase activity. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 53; SEQ ID NO: 55; SEQ ID NO: 57; and SEQ ID NO: 59. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence of SEQ ID NO: 53. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NO: 54; SEQ ID NO: 56; SEQ ID NO: 58; and SEQ ID NO: 60. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that encodes an amino acid sequence of SEQ ID NO: 54.

In various embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that: has at least 95% identity to SEQ ID NO: 1 over the entire length thereof; has at least five mutations of: a mutation at base 251 of CGC to CAC; a mutation at base 1240 of ATC to GTC; a mutation at base 1958 of GAT to GGT; a mutation at base 2092 from TGG to GGG; and a mutation at base 2203 from GTG to ATG; and encodes a polypeptide having RNA polymerase activity. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence of SEQ ID NO: 61. In some embodiments, the first polynucleotide sequence (R) comprises a nucleotide sequence that encodes an amino acid sequence of SEQ ID NO: 62.

In various embodiments, the lac Z polynucleotide (Z) comprises: a nucleotide sequence selected from group consisting of SEQ ID NO: 63 and SEQ ID NO: 65, or a variant having at least 95% identity thereof encoding a polypeptide having β -galactosidase activity; or a nucleotide sequence encoding a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 64 and SEQ ID NO: 66 and β -galactosidase activity, or a variant having at least 95% identity thereof and β -galactosidase activity. In some embodiments, the lac Z polynucleotide (Z) comprises a lac Z polynucleotide from *E. coli* strain BL21.

In various embodiments, the lac Y polynucleotide (Y) comprises: a nucleotide sequence selected from group consisting of SEQ ID NO: 67 and SEQ ID NO: 69, or a variant having at least 95% identity thereof encoding a polypeptide having β -galactoside permease activity; or a nucleotide sequence encoding a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 68 and SEQ ID NO: 70 and β -galactoside permease activity, or a variant having at least 95% identity thereof and having β -galactoside permease activity. In some embodiments, the lac Y polynucleotide (Y) comprises a lac Y polynucleotide from *E. coli* strain BL21.

In various embodiments, the wild-type lac control region (C) comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 71 and SEQ ID NO: 72, or a variant having at least 95% identity thereof having a functional CAP binding site, promoter, operator, and ribosome binding site.

In various embodiments, the first polynucleotide sequence (R) encodes a temperature-sensitive T7 RNA polymerase. In some embodiments, T7 promoter activation does not occur at about 37° C. but does occur at about 30° C.

Another aspect of the invention provides a mutant T7 RNA polymerase as an isolated polypeptide.

In various embodiments, the isolated polypeptide comprises a variant of a polypeptide of SEQ ID NO: 2 wherein, the variant polypeptide is at least 95% identical to SEQ ID NO: 2 over the entire length thereof; the variant polypeptide has at least two mutations at an amino acid residue position corresponding to SEQ ID NO: 2 selected from the group consisting of: amino acid residue 84, Arg to His; amino acid residue 414, Ile to Val; amino acid residue 653, Asp to Gly; amino acid residue 698, Trp to Gly; and amino acid residue 735, Val to Met; the variant polypeptide has RNA polymerase activity; the variant polypeptide has reduced rates of uninduced expression in a T7 expression system compared to a T7 RNA polymerase of SEQ ID NO: 2; and the variant polypeptide has about the same or greater rates of induced expression in a T7 expression system compared to a T7 RNA polymerase of SEQ ID NO: 2. In some embodiments, the isolated polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24; SEQ ID NO: 26; SEQ ID NO: 28; SEQ ID NO: 30; and SEQ ID NO: 32. In some embodiments, the isolated polypeptide comprises an amino acid sequence of SEQ ID NO: 32.

In some embodiments, the isolated polypeptide has at least three mutations at an amino acid residue position corresponding to SEQ ID NO: 2 selected from the group consisting of: amino acid residue 84, Arg to His; amino acid residue 414, Ile to Val; amino acid residue 653, Asp to Gly; amino acid residue 698, Trp to Gly; and amino acid residue 735, Val to Met. In some embodiments, the isolated polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 34; SEQ ID NO: 36; SEQ ID NO: 38; SEQ ID NO: 40; and SEQ ID NO: 42; SEQ ID NO: 44; SEQ ID NO: 46; SEQ ID NO: 48; SEQ ID NO: 50; and SEQ ID NO: 52. In some embodiments, the isolated polypeptide comprises an amino acid sequence of SEQ ID NO: 50.

In some embodiments, the isolated polypeptide has at least four mutations at an amino acid residue position corresponding to SEQ ID NO: 2 selected from the group consisting of: amino acid residue 84, Arg to His; amino acid residue 414, Ile to Val; amino acid residue 653, Asp to Gly; amino acid residue 698, Trp to Gly; and amino acid residue 735, Val to Met. In some embodiments, the isolated polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 54; SEQ ID NO: 56; SEQ ID NO: 58; and SEQ ID NO: 60. In some embodiments, the isolated polypeptide comprises an amino acid sequence of SEQ ID NO: 54.

In some embodiments, the isolated polypeptide has at least five mutations at an amino acid residue positions corresponding to SEQ ID NO: 2 of: amino acid residue 84, Arg to His; amino acid residue 414, Ile to Val; amino acid residue 653, Asp to Gly; amino acid residue 698, Trp to Gly; and amino acid residue 735, Val to Met. In some embodiments, the isolated polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 62.

Another aspect of the invention provides an isolated nucleic acid encoding an isolated polypeptide described above.

Other objects and features will be in part apparent and in part pointed out hereinafter.

BRIEF DESCRIPTION OF THE DRAWINGS

Those skill in the art will understand that the drawings, described below, are for illustrative purposes only. The drawings are not intended to limit the scope of the present teachings in any way.

FIG. 1 is a photograph showing colored protein indicator resulting from plasmid pWB536, which expresses the fast-maturing T3 form of DsRed (Bevis & Glick, 2002) on the vector plasmid pET11. Four flasks, of different shapes and containing different volumes of media, were incubated under equivalent conditions. For details regarding methodology, see Example 1.

FIG. 2 is a photograph of 5 ml samples from the flasks shown in FIG. 1, where the intensity of the red coloring is an indicator of expression level. For details regarding methodology, see Example 1.

FIG. 3 is a photograph showing initial screen of genomic constructs transformed with pWB536 in an experiment to determine if they are auto-inducible. The two tubes on the right are negative and positive controls. The last tube on the right is the standard strain BL21(DE3)(pWB536). Strain/tube number 3, found by PCR to have no RNA polymerase gene, also serves as a negative control. Tube number 7 is BL21-ZRY strain pWB456.7. For details regarding methodology, see Example 3.

FIG. 4 is a series of photographs showing uninduced (leaky) levels of expression, providing a comparison of WB456.7 ("tube 7") vs. BL21(DE3). FIG. 4A shows Medium PG (Studier, 2005; phosphate salts, glucose as carbon source). The +/−Ser experiment visible on the label showed no difference. Tube 3 in FIG. 4A is a negative control with no T7 RNA polymerase gene. Tubes 2, 6, and 8 in FIG. 4A represent unsatisfactory constitutive constructs. Tube 7 in FIG. 4A is strain pWB456.7. The tube on the right of FIG. 4A is BL21(DE3). All strains shown in FIG. 4A harbor pWB536. FIG. 4B shows Medium MGD, Studier's recommended uninduced medium, after overnight culture. Tubes in FIG. 4B are as described in FIG. 4A. Again, WB456.7 has lower leakiness than BL21(DE3). For details regarding methodology, see Example 3.

FIG. 5 is a photograph showing expression levels. The top quadrant of the plate contains strain BL21-A1 (Invitrogen). The left quadrant of the plate contains strain pWB456.7. The right quadrant of the plate contains BL21(DE3). The bottom quadrant of the plate contains unsatisfactory construct. Medium is LB agar using NZamine and yeast extract; 100 ug/ml Ticarcillin. FIG. 4 demonstrates that strain WB456.7 has a lower background expression on rich plates than BL21 (DE3) carrying the same expression plasmid pWB536. For details regarding methodology, see Example 3.

FIG. 6 is a photograph showing pairs of tubes labeled with their strain numbers WB466.nn. Odd tubes are uninduced (MGD medium). Even tubes are auto-induced (5052 medium). Outstanding performance is unexpectedly delivered by WB466.15, appearing as the seventh (uninduced) and eighth (auto-induced) tubes from the left. For details regarding methodology, see Example 4.

FIG. 7 is a photograph showing cured and then retransformed strain WB466.15. Odd numbered tubes (light-gray in color) are MGD medium, while dark-gray colored tubes are 5052 auto-induction medium. As shown in this figure, strain WB466.15 repeatedly exhibits surprisingly tight control. As such, the initial result was not a mutant of the plasmid, and the new phenotype is stable. For details regarding methodology, see Example 4.

FIG. 8 is a photograph that compares the host construct ZRY transductant (P1.466.15/WB453) to the closest competing host, IBL21-A1 (arabinose inducible) (Invitrogen) and to the standard BL21(DE3). G=MGD medium. L=5052 auto-induction medium. LA=5052+0.2% arabinose also to induce BL21-A1, as recommended by Invitrogen. For details regarding methodology, see Example 4.

FIG. 9 is a diagram depicting recombination results in insertion of the T7 RNA polymerase gene between Z and Y, while leaving the lac control region unchanged.

FIG. 10 depicts the designed intergenic regions of the BL21-ZRY genome. Numbering is that of the transforming PCR-product DNA. All lac operon sequence not shown was intended to be wild-type, but strain WB466.15 may have silent and/or beneficial mutations. Dotted lines indicate T7 phage homology while dashed lines indicate *E. coli* genome homology. The T7 phage DNA also has unplanned mutations, which may be silent or beneficial.

FIG. 11 is a photograph that demonstrates the behavior of the strain BL21(DE) in comparison to the improved behavior of ZRY strains WB466.15, WB477f and WB478e. Each strain is shown after growth in 3 different liquid media. The order of the media in each group is: MGD (non-inducing, Studier, 2005), 5050 (non-inducing) and 5052 (auto-inducing, Studier, 2005). For 5050 and 5052 media, the first "5" refers to 0.5% glycerol, the "05" refers to 0.05% glucose. The last digit in 5052 media refers to 0.2% lactose; in 5050 media there is no lactose, therefore the last digit is "0". FIG. 11 also contains a bar graph presenting quantified results (intensity of red indicator protein as red/green ratio) of the photograph pictured above it.

FIG. 12 shows photographs of four bacterial strains grown on three different types of solid agar media plates and at three different growth temperatures. The top row shows plates that were incubated at 30° Celsius, the middle row at 37 Celsius, and the bottom row at 42° Celcius. The different growth media are arranged by column. The first column shows bacteria growing on LB media, the second column shows bacteria growing on LB media supplemented with 0.2% glucose, the third column shows bacteria growing on LB media supplemented with 0.2% lactose. In all photographs, BL21 (DE3) is in the top left quadrant, strain WB466.15 is in the top right quadrant, strain WB478e is in the bottom left quadrant, and WB477f is in the bottom right quadrant. For details regarding methodology, see Example 10.

DETAILED DESCRIPTION

The present inventors have developed, in various aspects of the present teachings, a variant of the T7 expression system that is extremely tight (i.e., low levels of "leaky" basal non-induced expression), and yet, still auto-inducible.

The present invention is based, at least in part, on mechanistic information about the catabolite-insensitivity of the lac L8-UV5 promoter used for the T7 RNA polymerase gene. By providing a wild-type lac operon control region, and by inserting a polynucleotide encoding a T7 polymerase between lac Z and lac Y of the lac operon (i.e., a "ZRY" construct), full sensitivity to catabolite repression can be preserved and leakiness of the expression system (i.e., a "ZRY strain") can be reduced. A prokaryotic expression system utilizing a ZRY strain can be fully sensitive to catabolite repression and provides reduced leakiness and superior performance as compared to, for example, an expression system employing a T7 RNA polymerase under the control of the mutant lac L8-UV5 promoter. This high level of repression can be utilized, for example, to allow overproduction of proteins, including toxic proteins that were previously not tolerated, in *E. coli*.

Full expression of a target gene from an expression clone with a T7lac promoter requires both induction of T7 RNA polymerase and release of the lac repressor from its binding site in the T7lac promoter. Both events can be triggered by release of the lac repressor by, for example, addition of IPTG

or by the presence of lactose in the medium. But, like other prior art inducible promoter systems, auto-induction T7lac polypeptide expression systems have a residual level of activity or "leakiness", which can lead to the inappropriate transcription and expression of the gene being cloned under the control of the promoter. A significant fraction of gene products (proteins), especially eukaryotic gene products, which may be worthy subjects of molecular and medical research, are in fact toxic to a bacterial cell which has not evolved to tolerate these exogenous proteins. Inappropriate early expression of gene products (proteins) which are toxic to the *E. coli* cell can prevent the study of these proteins using the T7 expression system.

It has now been discovered that at least a part of the leakiness of the widely-used BL21(DE3) expression system is due to the catabolite-insensitive lac L8-UV5 promoter used for the T7 RNA polymerase gene (SEQ ID NO.: 72).

Provided herein is a variant of the T7 expression system, in which a polynucleotide encoding a T7 RNA polymerase is inserted between lac Z and lac Y of the lac operon (i.e., a "ZRY" construct). Thus is provided full sensitivity to catabolite repression and reduced leakiness of a system for expression of a target polypeptide. Also described herein is a method for producing a selected gene product in a host cell employing a ZRY construct. Such a system can be even further improved through incorporation of a polynucleotide encoding a mutant T7 RNA polymerase. Mutant T7 RNA polymerase polypeptides, and encoding polynucleotides, are also provided herein. Various embodiments of the mutant T7 RNA polymerase can further reduce uninduced levels of expression and/or achieve as good or better levels of induced expression, as compared to a wild type T7 RNA polymerase. Also provided herein are host prokaryotic cells comprising a ZRY construct (i.e., a "ZRY strain"). Such ZRY strains can comprise wild-type T7 RNA polymerase or mutant T7 RNA polymerases.

One aspect described herein is a T7 RNA polymerase mutant polypeptide, and polynucleotides encoding such. In some embodiments, the mutant T7 RNA polymerase provides for reduced rates of uninduced expression in a T7 expression system compared to a wild type T7 RNA polymerase. In some embodiments, the mutant T7 RNA polymerase provides for comparable rates of induced expression in a T7 expression system compared to a wild type T7 RNA polymerase. In some embodiments, the mutant T7 RNA polymerase provides for both reduced rates of uninduced expression and comparable rates of induced expression in a T7 expression system compared to a wild type T7 RNA polymerase. As an example, uninduced and/or induced rates of expression of the mutant T7 RNA polymerase can be compared to a wild type T7 RNA polymerase of SEQ ID NO: 2.

Mutant T7 RNA polymerase described herein can be used in ZRY constructs, transformed host cells, and expression systems also described herein. These mutant T7 RNA polymerases can further reduce rates of uninduced expression in ZRY expression systems as compared to those using a wild type T7 RNA polymerase. These mutant T7 RNA polymerases can provide comparable, or increased, rates of induced expression in ZRY systems as compared to those using a wild type T7 RNA polymerase.

Design, generation, and testing of the variant nucleotides, and/or their encoded polypeptides, having the above required percent identities to polynucleotide SEQ ID NO: 1 or polypeptide SEQ ID NO: 2 and retaining the required polymerase activity of the expressed protein is within the skill of the art. For example, directed evolution and rapid isolation of mutants can be according to methods described in references including, but not limited to, Link et al. (2007) Nature

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Reviews 5(9), 680-688; Sanger et al. (1991) Gene 97(1), 119-123; Ghadessy et al. (2001) Proc Natl Acad Sci USA 98(8) 4552-4557. Thus, one skilled in the art could generate a large number of nucleotide and/or polypeptide variants having, for example, at least 95-99% identity to the sequences T7 polymerase described herein and screen such for activity according to methods routine in the art. Generally, conservative substitutions can be made at any position so long as the required activity is retained.

"Highly stringent hybridization conditions" are defined as hybridization at 65° C. in a 6×SSC buffer (i.e., 0.9 M sodium chloride and 0.09 M sodium citrate). Given these conditions, a determination can be made as to whether a given set of sequences will hybridize by calculating the melting temperature (T_m) of a DNA duplex between the two sequences. If a particular duplex has a melting temperature lower than 65° C. in the salt conditions of a 6×SSC, then the two sequences will not hybridize. On the other hand, if the melting temperature is above 65° C. in the same salt conditions, then the sequences will hybridize. In general, the melting temperature for any hybridized DNA:DNA sequence can be determined using the following formula: $T_m = 81.5^\circ \text{ C} + 16.6(\log_{10}[\text{Na}^+]) + 0.41$ (fraction G/C content) - 0.63(% formamide) - (600/l). Furthermore, the T_m of a DNA:DNA hybrid is decreased by 1-1.5° C. for every 1% decrease in nucleotide identity (see e.g., Sambrook and Russel, 2006). In some embodiments, a mutant T7 RNA polymerase polynucleotide hybridizes under highly stringent conditions to a polynucleotide of SEQ ID NO: 1.

Nucleotide and/or amino acid sequence identity percent (%) is understood as the percentage of nucleotide or amino acid residues that are identical with nucleotide or amino acid residues in a candidate sequence in comparison to a reference sequence when the two sequences are aligned. To determine percent identity, sequences are aligned and if necessary, gaps are introduced to achieve the maximum percent sequence identity. Sequence alignment procedures to determine percent identity are well known to those of skill in the art. Often publicly available computer software such as BLAST, BLAST2, ALIGN2 or Megalign (DNASTAR) software is used to align sequences. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared. When sequences are aligned, the percent sequence identity of a given sequence A to, with, or against a given sequence B (which can alternatively be phrased as a given sequence A that has or comprises a certain percent sequence identity to, with, or against a given sequence B) can be calculated as: percent sequence identity = $X/Y \times 100$, where X is the number of residues scored as identical matches by the sequence alignment program's or algorithm's alignment of A and B and Y is the total number of residues in B. If the length of sequence A is not equal to the length of sequence B, the percent sequence identity of A to B will not equal the percent sequence identity of B to A.

Various embodiments provide mutant T7 RNA polymerase having at least about 80% identity to a wild type T7 RNA polymerase, such as the polypeptide of SEQ ID NO: 2, encoded by the polynucleotide of SEQ ID NO: 1. For example, a mutant T7 RNA polymerase can have at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identity to a wild type T7 RNA polymerase. Preferably, a mutant T7 RNA polymerase polypeptide has at least about 95% identity to polypeptide SEQ ID NO: 2. Preferably, a polynucleotide encoding a mutant T7 RNA polymerase has

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at least about 95% identity to polynucleotide SEQ ID NO: 1. The mutant T7 RNA polymerase retains RNA polymerase activity. In some embodiments, the mutant T7 RNA polymerase has reduced rates of uninduced expression and/or about the same or greater rates of induced expression in a T7 expression system compared to a T7 RNA polymerase of SEQ ID NO: 2.

Some embodiments of the mutant T7 RNA polymerase comprise at least one mutation at base 251, codon 84 (CGC to 10 CAC, and Arg to His, respectively); at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); at base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); at base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); or at base 2203, codon 735 (GTG to ATG, and Val to Met, respectively). For example, a mutant T7 RNA polymerase can comprise at least one mutation at base 251, codon 84 (CGC to CAC, and Arg to His, respectively) (e.g., SEQ ID NO: 3; SEQ ID NO: 4). As another example, a mutant T7 RNA polymerase can comprise at least one mutation at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively) (e.g., SEQ ID NO: 5; SEQ ID NO: 6). As another example, a mutant T7 RNA polymerase can comprise at least one mutation at base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively) (e.g., SEQ ID NO: 7; SEQ ID NO: 8). As another example, a mutant T7 RNA polymerase can comprise at least one mutation at base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively) (e.g., SEQ ID NO: 9; SEQ ID NO: 10). As another example, a mutant T7 RNA polymerase can comprise at least one mutation at base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 11; SEQ ID NO: 12).

Further embodiments of the mutant T7 RNA polymerase comprise at least two mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); at base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); at base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); or at base 2203, codon 735 (GTG to ATG, and Val to Met, respectively). It is understood that various embodiments can contain different combinations of the above mutations.

As an example, a mutant T7 RNA polymerase can include at least two mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively) and base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively) (e.g., SEQ ID NO: 13; SEQ ID NO: 14). As another example, a mutant T7 RNA polymerase can include at least two mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively) and base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively) (e.g., SEQ ID NO: 15; SEQ ID NO: 16). As another example, a mutant T7 RNA polymerase can include at least two mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively) and base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively) (e.g., SEQ ID NO: 17; SEQ ID NO: 18). As another example, a mutant T7 RNA polymerase can include at least two mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively) and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 19; SEQ ID NO: 20).

As another example, a mutant T7 RNA polymerase can include at least two mutations at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively) and base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively) (e.g., SEQ ID NO: 21; SEQ ID NO: 22). As another example, a mutant T7 RNA polymerase can include at least two mutations at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively) and base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively) (e.g., SEQ ID NO: 23; SEQ ID NO: 24). As

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another example, a mutant T7 RNA polymerase can include at least two mutations at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively) and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 25; SEQ ID NO: 26).

As another example, a mutant T7 RNA polymerase can include at least two mutations at base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively) and base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively) (e.g., SEQ ID NO: 27; SEQ ID NO: 28). As another example, a mutant T7 RNA polymerase can include at least two mutations at base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively) and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 29; SEQ ID NO: 30).

As another example, a mutant T7 RNA polymerase can include at least two mutations at base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively) and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 31; SEQ ID NO: 32).

Further embodiments of the mutant T7 RNA polymerase comprise at least three mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); at base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); at base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); or at base 2203, codon 735 (GTG to ATG, and Val to Met, respectively). It is understood that various embodiments can contain different combinations of the above mutations.

As an example, a mutant T7 RNA polymerase can include at least three mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); and base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively) (e.g., SEQ ID NO: 33; SEQ ID NO: 34). As another example, a mutant T7 RNA polymerase can include at least three mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); and base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively) (e.g., SEQ ID NO: 35; SEQ ID NO: 36). As another example, a mutant T7 RNA polymerase can include at least three mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); and base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively) (e.g., SEQ ID NO: 37; SEQ ID NO: 38).

As another example, a mutant T7 RNA polymerase can include at least three mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); and base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively) (e.g., SEQ ID NO: 39; SEQ ID NO: 40). As another example, a mutant T7 RNA polymerase can include at least three mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 41; SEQ ID NO: 42).

As another example, a mutant T7 RNA polymerase can include at least three mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEO ID NO: 43; SEO ID NO: 44).

As another example, a mutant T7 RNA polymerase can include at least three mutations at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); and base 2092,

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codon 698 (TGG to GGG, and Trp to Gly, respectively) (e.g., SEQ ID NO: 45; SEQ ID NO: 46). As another example, a mutant T7 RNA polymerase can include at least three mutations at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 47; SEQ ID NO: 48).

As another example, a mutant T7 RNA polymerase can include at least three mutations at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 49; SEQ ID NO: 50).

15 As another example, a mutant T7 RNA polymerase can include at least three mutations at base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g.,
20 SEQ ID NO: 51; SEQ ID NO: 52).

Further embodiments of the mutant T7 RNA polymerase comprise at least four mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); at base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); at base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); or at base 2203, codon 735 (GTG to ATG, and Val to Met, respectively). It is understood that various embodiments can contain different combinations of the above mutations.

30 As an example, a mutant T7 RNA polymerase can include at least four mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); and base 2092, codon 698 (TGG to CGG, and Trp to Gly, respectively) (e.g.

codon 698 (TGG to GGG, and Trp to Gly, respectively) (e.g., SEQ ID NO: 53; SEQ ID NO: 54). As another example, a mutant T7 RNA polymerase can include at least four mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); base 1958, codon 653 (GAT to GGT, and

Asp to Gly, respectively); and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 55; SEQ ID NO: 56). As another example, a mutant T7 RNA polymerase can include at least four mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); base

1240, codon 414 (ATC to GTC, and Ile to Val, respectively); base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 57; SEQ ID NO: 58). As another example, a mutant T7 RNA polymerase can include

and other example, in mutant 735, a poly A tail was found at least four mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); and base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (e.g., SEQ ID NO: 50, SEQ ID NO: 60).

SEQ ID NO: 59; SEQ ID NO: 60).

Further embodiments of the mutant T7 RNA polymerase comprise at least five mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); at base 1240, codon 60 414 (ATC to GTC, and Ile to Val, respectively); at base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); at base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); and at base 2203, codon 735 (GTG to ATG, and Val to Met, respectively). (e.g., SEQ ID NO: 61; SEQ ID NO: 62).

In some embodiments, the mutant T7 RNA polymerase is temperature-sensitive. In one embodiment, the mutant T7 RNA polymerase does not express a target polynucleotide

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sequence under control of a T7 promoter when grown at 37° Celsius, but the can express a target polynucleotide under the control of a T7 promoter when grown at 30° Celsius. This temperature-sensitive control of expression from the T7 promoter can be a desirable trait, and can allow increased control of the expression of genes regulated by the T7 promoter (see Example 10; Table 3; FIG. 12).

In some embodiments, the mutant T7 RNA polymerase is not a temperature-sensitive strain. In one embodiment, the mutant T7 RNA polymerase is capable of expressing a target polynucleotide under control of a T7 promoter when *E. coli* are grown at 37° Celsius. In another embodiment, mutant T7 RNA polymerase is capable of expressing a target polynucleotide under control of a T7 promoter when *E. coli* are grown at 42° Celsius. In another embodiment, the mutant T7 RNA polymerase is capable of expressing a target polynucleotide under control of a T7 promoter when *E. coli* are grown at 37° or 42° Celsius. The ability of a mutant T7 RNA polymerase to express a target polynucleotide from a T7 promoter when grown at the temperature at which *E. coli* are normally grown can be a desirable trait (see Example 10; Table 3).

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polymerase binds the DNA to begin transcription of the polycistronic lac mRNA. Immediately downstream (towards Lac Z) of the promoter is the operator region. This operator can be bound by Lac I to prevent transcription of the polycistronic lac mRNA. Lac I is constitutively present at low levels in the bacterial cell, and, in the absence of lactose, constitutively bound to the operator in the lac regulatory region. When lactose is present in the cell, Lac I preferentially binds the lactose, which causes a conformational change in the Lac I protein and the consequent release of Lac I from the lac regulatory region.

A polynucleotide encoding a T7 RNA polymerase (e.g., T7 gene 1, SEQ ID NO: 1) or a mutant T7 RNA polymerase (as described above) can be inserted between the lac Z and lac Y of the lac operon by a variety of means known to the art (see e.g., FIG. 9). For example, design and construction of a ZRY strain can be according to the gene transplacement method of Datsenko and Wanner (2000) (see e.g., Example 3). Other suitable methods will be known to those skilled in the art.

In some embodiments, the lac control region is a wild-type lac control region. The wild-type lac operon control region

TABLE 1

T7 polymerase nucleotides and polypeptide residues at specified position corresponding to SEQ ID NO: 1 and SEQ ID NO: 2, respectively, for various strains

	251/84 251/84	1240/414 1240/414	1958/653 1958/653	2092/698 2092/698	2203/735 2203/735
Wild type	CGC Arg	ATC Ile	GAT Asp	TGG Trp	GTG Val
WB466 .15	(WT)	GTC Val	(WT)	GGG Gly	ATG Met
WB477f	CAC His	GTC Val	GGT Gly	GGG Gly	(WT)
WB478e	(WT)	(WT)	(WT)	GGG Gly	ATG Met

Another aspect is a ZRY construct in which a polynucleotide encoding a T7 RNA polymerase or mutant T7 RNA polymerase occurs between a lac Z polynucleotide sequence encoding β-galactosidase and a lac Y polynucleotide sequence (Y) encoding a β-galactoside permease, forming ZRY. ZRY is downstream of a wild-type lac control region. In various embodiments, the lac control region comprises a CAP binding site, a promoter, an operator, and a ribosome binding site. In various embodiments, the promoter of the lac control region is a lac-inducible and catabolite-repressible promoter recognized by a host cell polymerase. In various embodiments, the polynucleotide encoding the T7 RNA polymerase or mutant T7 RNA polymerase is under the control of the lac-inducible and catabolite-repressible promoter of the lac control region.

Upstream of the coding region, there are sequences that regulate the expression of the polycistronic lac mRNA. The lac control region, or regulatory region, (see e.g., SEQ ID NO.: 71, SEQ ID NO.: 72) comprises a CAP binding site, a promoter, and an operator (O1). The lac control region also comprises a ribosome binding site (i.e., a Shine-Delgarno sequence). Furthest upstream from the Lac Z gene is the CAP binding site. The CAP binding site binds CAP protein and recruits *E. coli*'s endogenous RNA polymerase to the lac promoter. The promoter is downstream (towards Lac Z) of the CAP binding site. The promoter is the site at which the RNA

can reduce uninduced basal expression levels in the expression system. In some embodiments, the lac control region has a nucleotide sequence of SEQ ID NO: 71 or SEQ ID NO: 72. In some embodiments, the lac control region is a variant of SEQ ID NO: 71 or SEQ ID NO: 72 having at least 95% identity thereof having a functional CAP binding site, a promoter, an operator, and a ribosome binding site. In some embodiments, the lac control region comprises a the lac control region from *E. coli* strain BL21.

Strain BL21(DE3) was found in the present invention to have a non-canonical substitution within the lac regulatory region, at -1 of the transcription initiation site (see Example 3; SEQ ID NO. 72). In other *E. coli* strains in which this region has been sequenced, e.g. K12, this substitution does not exist (SEQ ID NO.: 71). In some embodiments, the substitution can be repaired, and thus is provided an improved regulation of expression of the lac operon (see Example 3; SEQ ID NO.: 71).

The Lac Z portion of the polycistronic lac mRNA encodes a β-galactosidase. Lac Z has been completely sequenced in many *E. coli* strains, including K12 (SEQ ID NO.: 63) and O157:H7 (SEQ ID NO.: 65). These nucleotide sequences encode polypeptides of SEQ ID NO.: 64 and SEQ ID NO.: 66, respectively.

In some embodiments, the lac Z polynucleotide comprises a nucleotide sequence of SEQ ID NO: 63 or SEQ ID NO: 65.

In some embodiments, the lac Z polynucleotide comprises a variant of SEQ ID NO: 63 or SEQ ID NO: 65 having at least 95% identity thereof encoding a polypeptide having β -galactosidase activity. In some embodiments, the lac Z polynucleotide comprises a nucleotide sequence encoding a polypeptide having an amino acid sequence of SEQ ID NO: 64 or SEQ ID NO: 65 and β -galactosidase activity, or a variant having at least 95% identity thereof and β -galactosidase activity. In some embodiments, the lac Z polynucleotide comprises a lac Z polynucleotide from *E. coli* strain BL21.

The Lac Y portion of the polycistronic lac mRNA encodes a β -galactoside permease. The Lac Y portion of the lac mRNA has been completely sequenced in many *E. coli* strains, including K12 (SEQ ID NO.: 67) and O157:H7 (SEQ ID NO.: 69). These polynucleotides encode proteins of SEQ ID NO.: 68 and SEQ ID NO.: 70, respectively.

In some embodiments, the lac Y polynucleotide comprises a nucleotide sequence of SEQ ID NO: 67 or SEQ ID NO: 69. In some embodiments, the lac Y polynucleotide comprises a variant of SEQ ID NO: 67 or SEQ ID NO: 69 having at least 95% identity thereof encoding a polypeptide having β -galactoside permease activity. In some embodiments, the lac Y polynucleotide comprises a nucleotide sequence encoding a polypeptide having an amino acid sequence of SEQ ID NO: 68 or SEQ ID NO: 70 and β -galactosidase activity, or a variant having at least 95% identity thereof and β -galactosidase activity. In some embodiments, the lac Y polynucleotide comprises a lac Y polynucleotide from *E. coli* strain BL21.

One aspect provides an expression system for producing a target polypeptide in a host cell. The expression system can comprise a T7 RNA polymerase or a mutant T7 RNA polymerase inserted between lac Z and lac Y, as described above. The expression system can further comprise a target promoter polynucleotide sequence recognized by the encoded T7 RNA polymerase, or mutant T7 RNA polymerase, of ZRY. The expression system can further comprise a target polynucleotide sequence encoding a target polypeptide, where the target polynucleotide sequence is under the control of the target promoter.

One aspect provides a prokaryotic host cell engineered to comprise a ZRY expression system. ZRY can be inserted into the host genome as an exogenous construct. Alternatively, ZRY can be engineered in the host genome from exogenous R and endogenous Z and/or Y elements.

The present invention can be used with a variety of suitable prokaryotic hosts. The ZRY portion can be genetically transferred to the host genome using, for example, the well-known method of P1 transduction. In some embodiments, the prokaryotic host is an *E. coli*. For example, suitable prokaryotic hosts include, but are not limited to, *E. coli* strains of BL21, C2566, DH1, DH4I, DH5, DH5I, DH5IF, DH5IMCR, DH10B, DH10B/p3, DH11S, C600, HB101, JM101, JM105, JM109, JM110, K38, MG1655, RR1, Y1088, Y1089, CSH18, ER1451, and ER1647. Other suitable hosts are known in the art (see e.g., Gellissen, ed. (2005) Production of Recombinant Proteins: Novel Microbial and Eukaryotic Expression Systems, Wiley-VCH, ISBN-10: 3527310363; Baneyx (2004) Protein Expression Technologies, Taylor & Francis, ISBN-10: 0954523253). Preferably, the host is a BL21 *E. coli* strain.

Expression vectors can be introduced into host cells using a variety of standard techniques known to the art (see, e.g., Sambrook and Russel (2006) Condensed Protocols from Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, ISBN-10: 0879697717; Ausubel et al. (2002) Short Protocols in Molecular Biology, 5th ed., Current Protocols, ISBN-10: 0471250929; Sambrook and Russel (2001) Molecular Cloning: A Laboratory Manual, 3d ed.,

Cold Spring Harbor Laboratory Press, ISBN-10: 0879695773). Such techniques include, but are not limited to, viral infection, calcium phosphate transfection, liposome-mediated transfection, microparticle-mediated delivery, receptor-mediated uptake, cell fusion, electroporation, and the like. The transfected cells can be selected and propagated to provide recombinant host cells that comprise the expression vector stably integrated in the host cell genome.

Host strains developed according to the approaches described herein can be evaluated by a number of means known in the art (see e.g., Studier (2005) Protein Expr Purif. 41(1), 207-234; Gellissen, ed. (2005) Production of Recombinant Proteins: Novel Microbial and Eukaryotic Expression Systems, Wiley-VCH, ISBN-10: 3527310363; Baneyx (2004) Protein Expression Technologies, Taylor & Francis, ISBN-10: 0954523253). For example, host strains can be conveniently tested for degree of control, leakiness of expression, and auto-induction capacity using a colorometric positive indicator, such as DsRed.T3 (see e.g., Examples 3, 5, 10). Furthermore, a colorometric positive indicator, such as DsRed.T3, can be employed to monitor auto-induction protocols employing strains described herein. As another example, luciferase can be used as an indicator (see Barnes, 1990). An advantage of luciferase is that no protein purification and concentration is necessary, and it can be assayed very sensitively (e.g., down to about one molecule per cell).

In one embodiment, the ZRY strain is WB456.7, which comprises a wild-type lac promoter and T7 polymerase gene 1 (SEQ ID NO: 1) inserted between lac Z and lac Y of the lac operon. Strain WB456.7 is privately deposited (available on request).

In one embodiment, the ZRY strain is WB466.15, which comprises a wild-type lac promoter and a mutant T7 polymerase gene (SEQ ID NO: 49) inserted between lac Z and lac Y of the lac operon. Strain WB466.15 is privately deposited (available on request). ZRY strain WB466.15 contains mutations at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); at base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); and at base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (SEQ ID NO: 49, SEQ ID NO: 50, respectively) (see Table 1).

In one embodiment of the invention, the ZRY strain is WB478e, which comprises a wild-type lac promoter and a mutant T7 polymerase gene (SEQ ID NO: 31) inserted between lac Z and lac Y of the lac operon. Strain WB478e is privately deposited (available upon request). ZRY strain WB478e contains mutations at base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively); and at base 2203, codon 735 (GTG to ATG, and Val to Met, respectively) (SEQ ID NO: 31, SEQ ID NO: 32, respectively) (see Table 1).

In one embodiment of the invention, the ZRY strain is WB477f, which comprises a wild-type lac promoter and mutant T7 polymerase gene (SEQ ID NO: 53) inserted between lac Z and lac Y of the lac operon. Strain WB477f is privately deposited (available upon request). Numbering from the first base of the ATG start codon of T7 gene 1 (SEQ ID NO: 1) which codes for T7 RNA polymerase (SEQ ID NO: 2), ZRY strain WB477f contains mutations at base 251, codon 84 (CGC to CAC, and Arg to His, respectively); at base 1240, codon 414 (ATC to GTC, and Ile to Val, respectively); at base 1958, codon 653 (GAT to GGT, and Asp to Gly, respectively); and at base 2092, codon 698 (TGG to GGG, and Trp to Gly, respectively) (SEQ ID NO: 53, SEQ ID NO: 54, respectively) (see Table 1).

In some embodiments, the ZRY strain is a temperature-sensitive strain. In one embodiment, the strain does not express a gene under control of the T7 promoter when grown

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at 37° Celsius, but the strain can express a gene under the control of the T7 promoter when grown at 30° Celsius. This temperature-sensitive control of expression from the T7 promoter can be a desirable trait, and can allow increased control of the expression of genes regulated by the T7 promoter (see Example 10; Table 3; FIG. 12).

In some embodiments, the ZRY strain is not a temperature-sensitive strain. In one embodiment, the strain is capable of expressing genes under control of the T7 promoter when *E. coli* are grown at 37° Celsius. In another embodiment, the strain is capable of expressing genes under control of the T7 promoter when *E. coli* are grown at 42° Celsius. In another embodiment, the strain is capable of expressing genes under control of the T7 promoter when *E. coli* are grown at 37° or 42° Celsius. The ability of a strain to express genes from the T7 promoter when grown at the temperature at which *E. coli* are normally grown can be a desirable trait (see Example 10; Table 3).

A ZRY strain can be utilized with a manual induction and/or auto-induction. An example of a manual induction system includes, but is not limited to, an expression system induced by the addition of IPTG. Preferably, the ZRY strain is utilized with an auto-induction expression system.

One aspect provides a method for producing a selected gene product in a host cell comprising a ZRY expression system. The ZRY construct, expression system, and host cell strain are as described above. The ZRY strain is engineered to express a target polypeptide of interest under control of a T7 promoter. As described above, a T7 RNA polymerase or mutant T7 RNA polymerase is inserted between lac Z and lac Y, and ZRY is downstream of a wild-type lac control region. The polynucleotide encoding the T7 RNA polymerase or mutant T7 RNA polymerase is under control of a lac-inducible and catabolite-repressible promoter of the wild-type lac control region. A target polynucleotide sequence encoding the target polypeptide is introduced into the host cell. The host cell comprising ZRY and the polynucleotide encoding the target polypeptide is incubated under conditions appropriate for expression of the T7 RNA polymerase and expression of the target polypeptide from the target polynucleotide sequence.

Protein production by auto-induction processes are well known in the art (see e.g., Studier (2005) *Protein Expr Purif.* 41(1), 207-234, incorporated herein by reference). Except as otherwise noted herein, therefore, the processes of the present invention can be carried out in accordance with such processes. Preferably, the auto-induction system utilizes the 5052 medium of Studier (2005) but a variety of other media known to the art can be utilized. For example, the medium need not contain any NZ amine nor yeast extract, for auto-induction in minimal medium, which allows more efficient labelling by special isotopes.

The improvements described herein are compatible with, and can therefore extend the anti-leak protection of, a variety of existing modifications to T7lac expression systems. For example, the various ZRY strain embodiments can be used with toxicity-resistant strains (e.g., Miroux & Walker, 1996; Lucigen); plasmid copy-number control for the T7 expression vector (e.g., pETcoco, Novagen); and additional lac operators to the pET vector series. As another example, a ZRY strain embodying comprising the wild-type T7 RNA polymerase can be used with coded inhibitors of the T7 RNA polymerase, such as T7 lysozymes (e.g., ancillary plasmids pLysS and pLysE).

Methods for expressing proteins in prokaryotic hosts are well-known to those of skill in the art (see e.g., Gellissen, ed. (2005) *Production of Recombinant Proteins: Novel Micro-*

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bial and Eukaryotic Expression Systems

10 Wiley-VCH, ISBN-10: 3527310363; Baneyx (2004) *Protein Expression Technologies*, Taylor & Francis, ISBN-10: 0954523253). One skilled in the art can adapt known methods for expressing proteins in prokaryotic hosts so as to incorporate aspects of the present invention. Generally, the expression method utilizes a T7 RNA polymerase and a T7lac promoter for control thereof. For example, the expression method can utilize a T7 RNA polymerase of SEQ ID NO: 2, encoded by SEQ ID NO: 10 1, or a variant thereof. As another example, the expression method can utilize a mutant T7 RNA polymerase, as described above.

Since some protein can be inactivated and/or insoluble in inclusion bodies at high, post-induction times, levels of protein at higher levels can be assessed in parallel on (total) protein gels to determine if they agree with the colorimetric or enzyme assays.

Isolation of expressed polypeptides can be according to methods known in the art (see e.g., Yakhnin et al., 1998). 20 Polypeptides expressed in bacteria such as *E. coli* may be retained in the cytoplasm, typically as insoluble granules, or directed to the periplasmic space by a bacterial secretion sequence. Granules can be recovered when the cells are lysed and denatured using, for example, guanidine isothiocyanate or urea. Denatured polypeptide can then be refolded and dimerized by diluting the denaturant, such as by dialysis against a solution of urea and a combination of reduced and oxidized glutathione, followed by dialysis against a buffered saline solution. Polypeptide can be recovered from the periplasmic space in a soluble and functional form by disrupting the cells (e.g., sonication or osmotic shock) to release the contents of the periplasmic space and recovering the protein.

As an example, proteins can be isolated and purified using ethanol M extraction in the presence of ammonium sulfate. 35 This method can be employed with a colorimetric indicator, such as DsRed.T3 protein, by lysing the cells with lysozyme and detergent rather than sonication. Also, at lower salt, the protein precipitates with ethanol without changing its spectral characteristics, providing an easy means to concentrate it.

Modifications of the nucleotide sequences or regulatory elements disclosed herein which maintain the functions contemplated herein are within the scope of this invention. Such modifications include insertions, substitutions and deletions, and specifically substitutions which reflect the degeneracy of 40 the genetic code.

All publications, patents, patent applications, and other references cited in this application are incorporated herein by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application or other reference was specifically and individually indicated to be incorporated by reference in its entirety for all purposes. Citation of a reference herein shall not be construed as an admission that such is prior art to the present invention.

Having described the invention in detail, it will be apparent that modifications, variations, and equivalent embodiments are possible without departing the scope of the invention defined in the appended claims. Furthermore, it should be appreciated that all examples in the present disclosure are provided as non-limiting examples.

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EXAMPLES

The following non-limiting examples are provided to further illustrate the present invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples that follow represent approaches the inventors have found function well in the practice of the invention, and thus

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can be considered to constitute examples of modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments that are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Example 1

Colored Protein Indicator

As a convenient and sensitive indicator of uninduced and induced expression levels, the plasmid pWB536 was constructed. Plasmid pWB536 expresses the fast-maturing T3 form of DsRed (Bevis & Glick, 2002) on the vector plasmid pET11 (Studier (1990)). A parallel control in a separate flask does not however ensure that a target protein culture is proceeding at the same pace, since some target proteins may compromise the metabolism of the cells when the expressed enzyme begins to appear. A single-copy indicator gene would more accurately reflect conditions inside the production cells, and would not excessively contaminate the preparation (compared to the target protein on a multi-copy plasmid).

Protein DsRed.T3 is fast-maturing (Bevis & Glick, 2002) and requires no additives; but fast-maturing as it is, it may be a lagging indicator, and/or it may have an odd dependence on the metabolism of the cell for proper maturation, which requires an oxidation step. Therefore, also tested was bacterial proteorhodopsin (which requires the addition of retinal for color maturation) as an alternate indicator. The clone was in a pET27b vector.

For current use of the DsRed indicator, the routine inoculation of an extra 500 ml flask with the expression strain carrying pWB536 is useful, with the same aeration (volume and shaking speed) as the flasks inoculated to express a research subject protein(s).

Even as a parallel culture in a separate flask, it was found that DsRed production by pWB536 is an illuminating control of whether conditions of time, temperature and aeration (culture volume) are adequate for good auto-induction. Studier (2005) did demonstrate and recommend workable flasks sizes (2.8 liter Fernbach), volume (500 ml), and shaking speed (350 rpm) and temperature (30° Celsius). But it has been found in the experiments described herein reasonable conditions that do not support auto-induction (e.g., 500 ml, 2 liter Erlynmeyer), where a ready color indicator is useful (see e.g., FIG. 2).

Demonstration of the use of this indicator gene is shown in FIG. 1. Four flasks (and a fifth not shown) were incubated under identical conditions (250 rpm, 30° C.) except for the shape of the flasks and the volume of auto-induction medium inoculated with pWB536/BL21(DE3). Flask A was 2.8 L Fernbach flask containing 1 L of medium; B was a 2.8 L Fernbach flask containing 500 ml of medium; C was a 2 L Erlynmeyer flask containing 500 ml of medium; D was a 2 L Erlynmeyer flask containing 1 L of medium; E was a 2 L Erlynmeyer flask with baffles containing 1 L of medium (see e.g., FIG. 1). The best expression level was the geometry recommended by Studier (2005) except no baffles (i.e., flask B) (see e.g., FIG. 2).

The bulk, visible-light color of the DsRed indicator can be used to assess expression levels. DsRed is also fluorescent, with excitation at both UV and 500 nm. A single rogue transcription event may allow the translation of several molecules of T7 RNA polymerase, resulting in perhaps hundreds of DsRed protein molecules being made. Therefore, when the expression system “leaks”, some cells may be very fluores-

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cent, and most will be dark. The “pop” of expression can then be diluted out as the cells divide. Single cells can be examined under a fluorescent microscope. Leakingness can be scored as fluorescent cells per thousand, or per 10,000.

Example 2

T7-Promoter/DsRed Gene

10 A T7-promoter/DsRed gene located near the lac operon is constructed and evaluated. The pT7-DsRed gene is inserted upstream of the lac operon, reading away from lacI (clockwise on the *E. coli* genome after 366734). The T7 terminator sequence from Studier's pET11 vector is included in an attempt to not disrupt the adjacent genes for propionate metabolism, only 77 bp away.

Example 3

Construction OF BL21-ZRY

Using BL21 DNA as a source of wild-type lac operon, a strain was constructed with map order Z,R,Y. The strain number is WB456. Unexpectedly, DNA sequence confirmation of 25 two independent constructs (WB456.7 and WB456.12) revealed an uncharacterized mutation (Gaaatt to Aaatt) at the base right before the start of mRNA transcription from the lac promoter. Additional DNA sequencing of DNA of parent strains determined that this mutation is present in the parental 30 BL21. This mutation represents a potential contributor to the uninduced background in the standard Studier system using BL21(DE3). Another source of lac DNA (λ plac5) was used to repeat the construction to see if the resulting strain exhibits noticeably tighter regulation.

35 Construction of BL21-ZRY proceeded in 2 phases, each using the gene transplacement method of Datsenko and Wanner (2000). This method uses PCR products with only ~40 bp of spanning homology on either side, but carrying a selectable marker. In brief, target bacteria carry plasmid pKD46 which 40 has a Ts-repliicon (therefore easily curable at 42 deg.) and which carries the recombination genes of phage lambda under arabinose control. Target bacteria are induced with 1 mM arabinose before they are made electrocompetent for transformation, so they can recombine with PCR product as shown in, for example, FIG. 9. The new DNA junction sequences are shown in, for example, FIG. 10. More detailed methodology is as follows.

Phase 1 of the construction of BL21-ZRY replaced the lacZ codons with a promoter and gene for kanamycin resistance, 50 leaving intact the lac promoter and lacY,A. The donor kanR PCR product had 47 bp of lac operon target DNA homology on the left (promoter) side, up to 2 bases before the lacZ start codon. On the downstream side of the lacZ gene, the donor KanR PCR product had 52 bases of homology with lacY 55 codons. It was amplified in 100 μ l from 2 ng pKD4 (Datsenko and Wanner) plasmid DNA as template using overlapping primers NotZKD4 (1 pmole) and LacZnot1 (20 pmoles) on the left, and unZKD4' (1 pmole) and LacZnot-100 (20 pmoles) on the right. The resulting strain was designated 60 WB448, was made lysogenic for P1CmClr100, and the temperature-induced P1 lysate was used and plated with citrate (Miller, 1970) to transduce BL21 to the phenotype of KanR and lac- to make the strain designated WB453.

Phase 2 of the construction of BL21-ZRY used selection 65 for growth on lactose as a carbon source to return lacZ to the operon in BL21, but now adjacent to T7 gene 1 (RNP) (SEQ ID NO: 1). The Z-RNP-Y amplicon was produced by over-

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lapping PCR from 3 individual PCR products. Amplicon 1 carried lacZ with the p-o region on the left, and 33 bp of T7 gene 1 DNA on the right; amplicon 2 was the T7 gene 1 (SEQ ID NO: 1) with 33 bases of lacZ DNA on the left and 33 bases of lacY on the right; amplicon 3 was 501 bases of lacY with 33 bases of T7 gene 1 (SEQ ID NO: 1) on the left. Each gene was designed to have or retain Shine-Dalgarno sequences and start and stop codons, with minimal intergenic regions (see e.g., FIG. 10). These amplicons were precipitated with PEG to remove PCR primers. The overlapping PCR assembly step employed primer lacI-end on the left and primer lacY'500 on the right, with all 3 amplicons (approximately 2 ng each) as template, and KlenTaqLA as the catalyzing DNA polymerase mixture (Barnes, 1994) at pH 7.9 to improve fidelity. The assembly (overlapping-) PCR exhibited a prominent product of the expected size (6.4 kb) in addition to several minor products. The whole PCR reaction was precipitated with PEG and approximately 200 ng of DNA was used for transformation without further purification. After transformation of WB453 (pKD46) previously induced with 1 mM arabinose (Datsenko and Wanner, 2000), and plating on lactose minimal (ML) plates, eight of 22 Lac+colonies (WB456.1-WB456.8) were picked for evaluation, and after purification these candidate strains were transformed with pWB536 to assess the presence of an inducible gene for T7 RNA polymerase. Four of the eight host strains could turn red after auto-induction in medium 5052 (see e.g., FIG. 3). One of these, WB456.7, exhibited the desired phenotype of lower expression than BL21(DE3) and BL21-Al on non-inducing media MG and MGD (see e.g., FIG. 4). Negative clone WB456.3, which was found (by whole-cell analytical PCR) to have no T7 RNP gene at all, was retained as a negative control.

The new strain, WB356.7, exhibits less leakiness in Studier's "uninducing" MGD medium compared to BL21(DE3), but the uninduced level is still detectable. The auto-induced level is at least, or greater than, that of BL21(DE3).

Example 4

Correction of BL21 SNP at Position-1 and Generation and Phenotype of WB466.15

As described above, the WB456.7 construct inherited from BL21 a non-canonical variant at position-1, right before the start of transcription at the lac promoter.

The construction was repeated using λ lacZ as the source of lac control region and lacZ to make WB466. FIG. 6 shows pairs of cultures, MGD (non-inducing) and 5052 (auto-inducing). DNA sequencing shows that each of these strains had corrected the non-canonical base in the lac control region. But most still leaked in MGD. Although a BL21(DE3) and WB456.7 controls are not shown, it is thought that the non-canonical mutation is silent.

FIG. 6 also demonstrates that strain WB466.15 is off in MGD yet induces in 5052 medium. The plasmid was cured from WB466.14 (pWB536) and reintroduced (i.e., retransformed), and 4/4 transformants behave in the same desirable way (see e.g., FIG. 7). Curing the strain was straightforward as it grows as red colonies on LB+lactose agar (or lactose+glucose minimal agar) without antibiotic, yet about 1% of the colonies are colorless, and prove to be cured and retransferrable to the same phenotype. Simple replica plating of bacteria grown without antibiotic gives rise to the same frequency of cured WB466.15. The left 2 strains in FIG. 7 were cured by the latter method, and the right 2 strains were cured by the lactose agar method.

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These results show that the initial result was not a mutant of the plasmid, and that the new WB466.15 phenotype is stable.

FIG. 8 compares the host construct to the closest competing host, BL21-Al (arabinose inducible) (Invitrogen) and to the standard BL21(DE3). Surprisingly, BL21-Al reproducibly shows leaky expression in Studier's non-inducing MGD medium, almost to the extent of BL21(DE3). WB471 is the first P1 transductant.

WB466.15 shows temperature-sensitive expression of T7-DsRed (construct described in Example 2). WB466.15 does not express DsRed from the pT7-DsRed construct when grown at 37° Celsius, but does induce its expression at 30° Celsius.

It is thought that the performance phenotype maps close to the ZRY operon.

Example 5

Mapping of WB466.15

Mutant strain WB466.15 was generated as described above.

Strain WB466.15 is mapped first by P1 transduction which determines whether the advantageous phenotype is linked to the ZRY operon. The PCR recombination/transduction is repeated using WB466.15 DNA (SEQ ID NO: 49) as template, to answer whether the mutant(s) map to the 6433 bp of the PCR construct. The 6.4 kb construct is sequenced, beginning with the T7 gene 1 portion. If one or more non-canonical changes are found, each are re-introduced one at a time into the ZRY background. As described above, these genomic modifications of 6.4 kb are by application of the Datsenko & Wanner method, using strain WB453(pKD46), which could as well be named BL21(kan: Δ lacZ)(pKD46), as host recipient for the transduction/recombination.

On identification of mutability of the T7 RNA polymerase, additional forward mutations are created by using mutagenic PCR. While the least mutagenic conditions were used for the construction shown in FIG. 9, it required 30 cycles to amplify the T7 gene 1, then 18 more for the overlapping PCR assembly step, so that gene 1 underwent 48 cycles of PCR in total.

To screen for more mutations, a replica plating strategy can be employed. It has been observed that, surprisingly, there is not any deleterious growth effect, or selection, against cells which are expressing the indicator DsRed from the plasmid pWB536, in strain WB466.15 growing in the presence of lactose. The strains can even grow on lactose minimal medium with less than 1% segregation. In contrast, on lac minimal medium, BL21(DE3) segregates (loses the plasmid) at much higher frequency. Therefore the recombination in FIG. 9 is carried out in a background that already contains pWB536 (and also pKD119, a tetR version of pKD46). It is expected that not only will the recombinants be Lac+, they will be red. But on rich plates without glucose nor lactose that are left for 5 days, WB466.15(pWB536) cells refuse to turn red, yet hosts BL21(DE3) and even, 2 days later, WB456.7, do turn some color. New mutants in the class of WB455.15 are expected to be easy to screen for by replica plating.

If the mutation for very low leakiness is not linked to the ZRY operon, it is possible that a chromosomal rearrangement such as an inversion is responsible, since inversions occur in cultures of *E. coli* and *Salmonella* at high frequency (Schmid & Roth, 1983). The latter reference provides guidance for mapping an inversion.

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Example 6

Assessment of Performance Compared to Other Expression Systems

Measurement of the control ratio over the time of auto-induction can assess the effectiveness of the various T7-expression systems versus the improvements described herein as well as those employed by others. The expression at a culture “time” of OD=1 or 2, during the glucose-utilizing phase before auto-induction, may be the most relevant to measure, vs. the final target protein level.

To increase our sensitivity and precision of detection of DsRed from uninduced cultures and auto-induction time points, the protein is purified, concentrated as necessary, and the absorbance read with a spectrophotometer or, more sensitively, the fluorescence with a fluorimeter. A ready purification method (shown for GFP by Yakhnin et al., 1998) involves ethanol extraction in the presence of 2.8 M ammonium sulfate. This method has been used effectively on DsRed.T3 protein, lysing the cells with lysozyme and detergent instead of the sonication used by Yakhnin et al. Also, at lower salt, the protein precipitates with ethanol without changing its spectral characteristics, providing an easy means to concentrate it.

As an alternate enzyme activity to assay precisely, β -galactosidase, as others have used for an analogous study (Setkas & Szybalski), is not used because β -galactosidase is used as part of auto-induction, upstream of the expression to be measured. CAT is avoided, because of the possibility of including the chloramphenicol-resistant plasmids pLysS and pLysE in these studies. Luciferase can be used (see Barnes, 1990). The advantage of luciferase is that no protein purification and concentration is necessary, and it can be assayed very sensitively (down to one molecule per cell at least).

Example 7

Generation and Phenotype of WB477f

The following example describes generation of WB477f and the resultant phenotype. Methods are according to those described in Examples 1-4, unless indicated otherwise. WB477f contains wild-type sequence upstream of the lac coding region.

Four bacterial strains were each grown in three different culture media (see e.g., FIG. 11). The culture media are MGD (non-inducing), 5050 (non-inducing) and 5052 (auto-inducing) (see e.g., FIG. 11, from left to right, respectively). BL21 (DE) (see e.g., left-most tube in FIG. 11) shows leakiness in both of the non-inducing media (first and second tube on the left, evidenced by the light and medium gray color of the cultures), and robust induction in the auto-inducing medium (evidenced by the darker gray color of the culture). The second set of three cultures shows WB466.15 (fourth, fifth and sixth tubes from the left, see e.g., Example 4), which shows excellent repression in non-inducing media and robust induction in auto-inducing media. The third set of cultures (seventh, eighth and ninth tubes from the left) demonstrates that WB477f shows no induction of the T7 promoter in MGD and 5050 non-inducing media and robust auto-induction in 5052 media. The dark gray color seen in the culture of WB477f grown in 5052 media (ninth tube from the left) shows that the newly invented strain WB477f performs as well or better in auto-inducing media than BL21(DE).

WB477f also shows tight control of auto-induction when grown on agar media. When WB477f is grown on standard

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LB-agar growth medium with ticarcillin, there is no induction of DsRed.T3 even after days of growth. In contrast, BL21 (DE) shows induction of DsRed.T3 after only two days of growth (data not shown).

WB477f shows robust auto-induction at temperatures up to 42° Celsius.

It is thought that the performance phenotype described in this example maps close to the ZRY operon.

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Example 8

Generation and Phenotype of WB478e

The following example describes generation of WB478e and the resultant phenotype. Methods are according to those described in Examples 1, 2, 3 and 4, unless indicated otherwise.

The bacterial strains were grown as follows: strain WB478e grown in MGD (non-inducing), 5050 (non-inducing), and 5052 (auto-inducing) media (right-most three cultures) (see e.g., FIG. 11). Results showed that strain WB478e represses expression from the T7 promoter in non-inducing media and induces T7-driven expression of DsRed.T3 in auto-inducing medium (see e.g., FIG. 11).

As described in Example 6, BL21(DE) shows a leaky phenotype in both of the non-inducing media and robust induction in the auto-inducing medium (first three tubes from the left in FIG. 11). The dark gray color of WB478e grown in auto-inducing medium demonstrates that this newly invented strain performs as good or better in these culture conditions than strain BL21(DE).

WB478e also shows tight control of auto-induction when grown on agar media. When WB478e is grown on standard LB-agar growth medium with ticarcillin, there is no induction of DsRed.T3 even after days of growth. In contrast, BL21 (DE) does show induction of DsRed.T3 after only two days of growth (data not shown).

WB478e shows temperature-sensitive expression of pT7-DsRed (construct described in Example 2). WB478e does not express DsRed from the pT7-DsRed construct when grown at 37° Celsius, but does induce its expression at 30° Celsius (data not shown).

It is thought that this performance phenotype maps close to the ZRY operon.

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Example 9

Objective Analysis of Amount of DsRed in Various Strains Grown in Various Liquid Culture Conditions

Described below is analysis of amount of DsRed in various strains grown liquid culture conditions. Use of DsRed results in colorimetric indications of expression level. Calculation of a red/green ratio from this data allows quantitative comparison of the amount of the red indicator protein DsRed.T3 (see e.g., FIG. 11).

To calculate the red/green ratio, a 21x21 square of pixels from the approximate center of an image of a culture was chosen. This image was evaluated by first scoring the red or green value of each individual pixel (range from 0 to 255). Then it was determined whether each pixel had a color value in the selected channel (either red or green) that was within ± 5 of each of the other 440 pixels in the selected area. If the pixel being evaluated was within ± 5 of this pixel for red, green and blue, it had a point added to its “similarity score.” The same protocol was repeated for the evaluation of that pixel in reference to each of the other 440 pixels in the selected area. This

evaluation was then repeated for each pixel in reference to every other pixel in the selected area for both color channels. After this evaluation, the pixel with the highest similarity score in each color channel was selected, and used as the representative red or green color of the selected area. Then all pixels with color scores within ± 5 of that value were averaged to find the average red and green values in the selected area.

The red/green ratio for each selection was calculated by dividing the average calculated red value by the average calculated green value. To remove background noise from the calculation, a gray area in the upper right of the photo was chosen, and its red/green ratio was calculated. The red/green ratio of the background area was 1.09. That value was subtracted from the ratio that was calculated for the selection from each culture.

Example 10

Objective Analysis of the Amount of DsRed in Various Culture Strains Grown on Various Solid Media

Almost every bacterial strain used in laboratory research is at some point propagated by growth in a culture plate that contains solidified agar medium. Strains BL21(DE3), WB466.15, WB477f, and WB478e were grown on three types of solid media and evaluated for the amount of DsRed.T3 that they express. Both inducing and non-inducing conditions were used. The strains were grown on regular LB medium, a standard *E. coli* growth medium. This medium should not induce expression of DsRed.T3. The strains were also grown on LB+0.2% glucose. This also should be a non-inducing medium. Further, the strains were grown on LB+0.2% lactose; this is the only culture condition which should induce transcription of the T7 polymerase gene 1 and therefore expression of DsRed.T3. The amount of DsRed.T3 expression was evaluated by the same calculation as described in Example 9, except that the subtracted background color value for this data was 1.079.

Results showed that strain BL21(DE3) has a significant amount of leaky induction when grown in LB medium, but the mutant strains show a very low level of expression of DsRed.T3 (see e.g., Table 2).

TABLE 2

Induction of strains at 30°, 37°, and 42° C. on non-inducing LB media				
LB media (non-inducing)	BL21(DE3)	WB466.15	WB477f	WB478e
30 Celsius	3.41	0.08	0.15	0.15
37 Celsius	3.63	0.09	0.06	0.13
42 Celsius	2.03	0.09	0.09	0.14

Results also showed a similar result when the strains were grown in LB+0.2% glucose media (see e.g., Table 3). This medium should not induce expression of DsRed.T3; yet strain BL21(DE3) shows robust red color, whereas the mutant strains have significantly less expression of DsRed.T3.

TABLE 3

Media with glucose (non- inducing)	Induction of strains at 30°, 37°, and 42° C. on non-inducing media with glucose			
	BL21(DE3)	WB466.15	WB477f	WB478e
30 Celsius	1.04	0.03	0.13	0.07
37 Celsius	1.46	0.08	0.12	0.12
42 Celsius	1.45	0.08	0.1	0.13

Results also showed that strain BL21(DE) exhibited expected induction of DsRed.T3 expression when bacteria are grown on LB+0.2% lactose medium (see e.g., Table 4). Similarly, strains WB466.15, WB477f and WB478e also show robust induction of DsRed.T3 expression when grown on media in these conditions (see e.g., Table 4).

TABLE 4

Media with lactose (inducing)	Induction of strains at 30°, 37°, and 42° C. on inducing media with lactose			
	BL21(DE3)	WB466.15	WB477f	WB478e
30 Celsius	0.46	1.54	2.19	2.52
37 Celsius	1.18	0.11	3.02	0.21
42 Celsius	0.76	0.13	0.63	0.19

Taken together, these results show that bacterial strains comprising the mutant T7 polymerase genes described herein show a tighter regulation of the expression of DsRed.T3 from the pT7-DsRed construct than the BL21(DE3) strain.

Also shown is that expression of DsRed.T3 in strains WB466.15 and WB478e is further able to be controlled by the temperature at which the strains are grown (see e.g., Table 3). Even when these strains are grown in inducing medium (i.e., with lactose), if the strains are grown at temperatures above 30 Celsius, there is essentially no expression of DsRed.T3. This data shows the expression of proteins in a pT7 construct can be even more tightly controlled through the use of these temperature sensitive variants.

FIG. 12 shows the experimental data from which Tables 2-4 were derived. FIG. 12 shows the photographs of four bacterial strains grown on three different types of solid agar media plates and at three different growth temperatures. The top row shows plates that were incubated at 30° Celsius, the middle row at 37 Celsius, and the bottom row at 42 Celcius. The different growth media are arranged by column. In all photographs, BL21(DE3) is in the top left quadrant, strain WB466.15 is in the top right quadrant, strain WB478e is in the bottom left quadrant, and WB477f is in the bottom right quadrant. Panel I of FIG. 12 has a technical error in the streaking of cells, where the upper half of the top right quadrant is actually BL21(DE3) cells, and therefore is red and appears induced. But the red indication in the upper half of the top right quadrant is a result of contamination from the top left quadrant of the plate.

Results showed that, when grown on LB or LB+glucose agar media plates, strain BL21(DE3) shows an extremely red phenotype, i.e., that T7 RNA polymerase expression is not adequately repressed in this strain on non-inducing conditions. In contrast, strains WB466.15, WB478e, and WB477f show very little (if any) red color when grown on either LB or LB+glucose media (first or second columns, non-inducing conditions). Nevertheless, when these strains are grown on

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LB+lactose media (third column, inducing condition), at 30° Celsius (panel C), they all show a robust red phenotype, indicating expression of T7 RNA polymerase gene 1 and consequent expression of DsRed.T3.

Panels F and I of FIG. 12 also demonstrate that strains WB466.15 and WB478e show temperature-sensitivity in

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their ability to transcribe T7 RNA polymerase gene 1, i.e., these two strains do not acquire a red color when grown at 37° Celsius or 42° Celsius. Strain WB477f is able to transcribe T7 RNA polymerase gene 1 at both 37 Celsius and 42 Celsius, demonstrating that it is not temperature sensitive in the regulation of this gene's expression.

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Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys		
565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn		
580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys		
595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly		
610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly		
625	630	635
Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln		
645	650	655
Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln		
660	665	670
Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr		
675	680	685
Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys		
690	695	700
Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg		
705	710	715
Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp		
725	730	735
Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu		
740	745	750
Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu		
755	760	765
Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His		
770	775	780
Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu		
785	790	795
Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr		
805	810	815
Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met		
820	825	830
Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln		
835	840	845
Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu		
850	855	860
Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe		
865	870	875
		880

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Ala Phe Ala

<210> SEQ ID NO 5
<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 5

atgaacacgca ttaacatcgca taagaacgac ttctctgaca tcgaactggc tgctatcccg	60
ttcaacactc tggctgacca ttacggtagcg cgtttagctc gccaacagg ggcccttgag	120
catgagtctt acgagatggg tgaagcacgc ttccgcaaga tgtttggcg tcaactaaa	180
getggtgagg ttgcggataa cgctgccgaa aagcctctca tcactaccct actccctaag	240
atgattgcac gcatcaacgca ctgggtttagcg gaagtgaaag ctaagcgccg caagcgcccg	300
acagccttcc agttcctgca agaaatcaag ccggaagccg tagcgtacat caccattaag	360
accactctgg ttgcgcttaac cagtgcgtac aatacaaccg ttcaaggctgt agcaagcgca	420
atcggtcggg ccattgagga cgaggctcgca ttccggcgta tccgtgaccc tgaagctaa	480
cacttcaaga aaaacgttga ggaacaactc aacaagcgcc tagggcacgt ctacaagaaa	540
gcatttatgc aagttgtcgaa ggctgacatg ctctctaaagg gtctactcg tggcgaggcg	600
tggcttcgtt ggcataagga agactctatt catgttaggg tagcgtcat cgagatgtc	660
attgagtcaa ccggaatggt tagtttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcgca acctgaatac gctgaggctca tcgcaaccgg tgcagggtcg	780
ctggctggca tctctccgat gttccaaacct tgcgttagttc ctccctaaaggc gtggactggc	840
attactgggt gtggcttattt ggctaacgggt cgctgcgttcc tggcgctgg tgcgtactcac	900
agtaagaaaag cactgatgcg ctacgaagac gtttacatgc ctgagggtta caaagcgatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaaatc tccctagggcg ccacgtaa	1020
atcaccaagt ggaagcattt tccggctcgag gacatccctg cgatttggcg tgaagaactc	1080
ccgatgaaac ccgaagacat cgacatgaat cctgaggctc tcaccggctg gaaacgtgct	1140
gccgctgctg tgtaccgcaaa ggacaaggct cgcaagtctc gccgtatcag ctttgagg	1200
atgcgttgcg aagccataaa gtttgcatac cataaggccg tctgggtccc ttacaacatg	1260
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggtt aggaaggta ctactggctg	1380
aaaatccacg gtgcacaaactg tgcgggtgtc gataagggtt cgttccctga ggcacatcaag	1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgtca agtctccact ggagaacact	1500
tgggtggctg agcaagattt tccgttctgc ttcccttgcgt tctgcttgcgt tgcgttggg	1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcggttgc cgggtctgc	1620
tctggcatcc agcacttctc cgcgatgcgtc cgagatgggg taggtggctcg cgccggtaac	1680
ttgcttccata gtgaaaccgt tcaggacatc tacgggattt tggctaaaggaa agtcaacgag	1740
attctacaag cagacgcaat caatgggacc gataacgaa tagttaccgt gaccgtatgg	1800
aacactgggt aaatctctga gaaaggtaag ctgggcacta aggcaactggc tggtaatgg	1860
ctggcttacg gtgttactcg cagtgtgtact aagcgttgcgt tcatgtacgt ggcttacggg	1920
tccaaagagt tcggcttcccg tcaacaagtg ctggaaagata ccattcagcc agctattgtat	1980
tccggcaagg gtctgtatgtt cactcagccg aatcaggctg ctggatacat ggctaaatgt	2040

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atttggaaat ctgtgagcgt gacgggtggta gctgcggttg aagcaatgaa ctggcttaag 2100
 tctgctgcta agctgctggc tgctgaggtc aaagataaga agactggaga gattttcg 2160
 aagcggtgcg ctgtgcattg ggtaactcct gatggttcc ctgtgtggca ggaatacaag 2220
 aagcctattc agacgcgcctt gaacctgtat ttccctcggtc agttccgcctt acagectacc 2280
 attaacacca acaaagatag cgagattgtat gcacacaaaac aggagtctgg tatcgctcct 2340
 aactttgtac acagccaaga cggtagccac cttcgtaaat ctgttagtgg ggcacacgag 2400
 aagtacggaa tcgaatcttt tgcactgatt cacgactcct tcggtaccat tccggctgac 2460
 gctgcgaacc tgttcaagc agtgcgcgaa actatggttg acacatatga gtcttgat 2520
 gtactggctg atttctacga ccagttcgctt gaccagttgc acgagtctca attggacaaa 2580
 atgcccacac ttccggctaa aggttaacttg aacctccgtg acatcttgc gtcggacttc 2640
 gcgttcgcgt aa 2652

<210> SEQ_ID NO 6
 <211> LENGTH: 883
 <212> TYPE: PRT
 <213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 6

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
 1 5 10 15
 Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
 20 25 30
 Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
 35 40 45
 Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
 50 55 60
 Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
 65 70 75 80
 Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
 85 90 95
 Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
 100 105 110
 Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
 115 120 125
 Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
 130 135 140
 Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 145 150 155 160
 His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
 165 170 175
 Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 180 185 190
 Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 195 200 205
 Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 210 215 220
 Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 225 230 235 240
 Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
 245 250 255
 Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val

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260	265	270
Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly		Tyr Trp Ala
275	280	285
Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala		
290	295	300
Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile		
305	310	315
Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala		
325	330	335
Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile		
340	345	350
Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp		
355	360	365
Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val		
370	375	380
Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe		
385	390	395
Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe		
405	410	415
Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe		
420	425	430
Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys		
435	440	445
Gly Lys Pro Ile Gly Lys Glu Gly Tyr Trp Leu Lys Ile His Gly		
450	455	460
Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys		
465	470	475
Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro		
485	490	495
Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu		
500	505	510
Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr		
515	520	525
Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln		
530	535	540
His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Arg Ala Val Asn		
545	550	555
Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys		
565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn		
580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys		
595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly		
610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly		
625	630	635
Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln		
645	650	655
Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln		
660	665	670
Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr		
675	680	685

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49

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<210> SEQ_ID NO 7
<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 7

atgaacacga ttaacatcg^c taagaacgac ttctctgaca tcgaactggc tgctatccg 60
ttcaacac^t tggctgacca ttacggtag cgtttagtc ggcacagtt ggccattgag 120
catgagtctt acgagatggg tgaagcacgc ttccgcaaga tgtttgagcg tcaactaaa 180
gtcggtgagg ttgcggataa cgctgccgc aagcctctca tcaactaccct actccctaag 240
atgattgcac gcatcaacga ctggttttag gaagtaaaa gtaagcgcgg caagcgcgg 300
acagccttcc agttctcg^a agaaaatcaag ccggaagccg tagcgtacat caccattaag 360
accactctgg ctgccttaac cagtgc^tgac aatacaaccg ttcaaggctgt agcaagcgc^a 420
atcggtcggg ccattgagga cgaggctcg^c ttccggcgta tccgtgac^c tgaagctaag 480
cacttcaaga aaaacgttga ggaacaactc aacaagcgcg tagggcacgt ctacaagaaa 540
gcatttatgc aagttgtcg^a ggctgacatg ctctctaagg gtctactcg^t tggcgaggcg 600
tggcttcgt^c ggcataagga agactctatt catgttaggg tacgctgcat cgagatgctc 660
attgagtc^a ccggaatgg^t tagttacac cgccaaaatg ctggcgtagt aggtcaagac 720
tctgagacta tcgaactcg^c acctgaatac gctgaggcta tcgcaacccg tgcagg^tg^c 780
ctggctggca tctctccgat gttccaaacct tgcgttagtc ctccctaagcc gtggactggc 840
attactggtg gtggctat^t ggctaacgg^t cgtcg^tc^t tggcgctgg^t gcgtactcac 900
actaaqa^aaaq cactqatqcc ctacqaaqac qtttacatqc ctqaaqqtqta caaadqcatt 960

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aacattgcgc	aaaacaccgc	atggaaaatc	aacaagaaag	tccttagcggt	cggcaacgta	1020
atcacaagg	ggaaggcattg	tccggtcgag	gacatccctg	cgattgagcg	tgaagaactc	1080
ccgatgaaac	cggaagacat	cgacatgaat	cctgaggctc	tcaccgctg	gaaacgtgct	1140
gccgctgctg	tgtaccgcaa	ggacaaggct	cgcaagtctc	gccgtatcag	ccttgagttc	1200
atgcttgagc	aagccaataa	gttgctaacc	cataaggcca	tctggttccc	ttacaacatg	1260
gactggcg	gtcgtgttta	cgcgtgtca	atgttcaacc	cgcaaggtaa	cgatatgacc	1320
aaaggactgc	ttacgctggc	gaaaggtaaa	ccaatcggt	aggaaggta	ctactggctg	1380
aaaatccacg	gtgcaaactg	tgcgggtgtc	gataaggttc	cgttccctga	gcatcaag	1440
ttcattgagg	aaaaccacga	gaacatcatg	gcttgcgct	agtctccact	ggagaacact	1500
tggggctgt	agcaagattc	tccgttctgc	ttccttgcgt	tctgcgttga	gtacgctgg	1560
gtacagcacc	acggcctgag	ctataactgc	tccctccgc	tggcggttga	cgggtcttgc	1620
tctggcatcc	agcacttctc	cgcgtatgctc	cgagatgagg	tagtggctcg	cgggttaac	1680
ttgcttcata	gtgaaaccgt	tcaggacatc	tacgggat	ttgctaagaa	agtcaacgag	1740
attctacaag	cagacgcaat	caatggacc	gataacgaa	tagttaccgt	gaccgatgag	1800
aacactgggt	aaatctctg	gaaagtcaag	ctgggcacta	aggcactggc	tggtaatgg	1860
ctggcttacg	gtgttactcg	cagtgtgact	aagcgttcag	tcatgacgct	ggcttacggg	1920
tccaaagagt	tccggcttccg	tcaacaagtg	ctggaaaggta	ccattcagcc	agcttattgat	1980
tccggcaagg	gtctgtatgtt	cactcagccg	aatcaggctc	ctggatacat	ggctaaagctg	2040
atttggaaat	ctgtgagcgt	gacgggtggta	gctgcgggtt	aagcaatgaa	ctggcttaag	2100
tctgctgcta	agctgctggc	tgctgaggctc	aaagataaga	agactggaga	gattctcgc	2160
aagcgttgcg	ctgtgcattt	ggtaactctt	gatggttcc	ctgtgtggca	ggaataacaag	2220
aagcctattc	agacgcgc	ttcacctgtat	ttcctcggtc	agttccgc	acagcctacc	2280
attaacacca	acaaagatag	cgagattgtat	gcacacaac	aggagtctgg	tatcgctcct	2340
aactttgtac	acagccaaga	cggttagccac	cttcgtaaaga	ctgttagtgc	ggcacacgag	2400
aagtacggaa	tgcataatctt	tgcactgatt	cacgactct	tccggatccat	tccggctgac	2460
gtgcgaacc	tgttcaaagc	agtgcgcgaa	actatggtt	acacatatga	gtcttgat	2520
gtactggctg	atttctacga	ccagttcgct	gaccagtgc	acgagtctca	attggacaaa	2580
atgccagcac	ttccggctaa	aggtaacttg	aacctccgt	acatctttaga	gtcggacttc	2640
gcgttgcgt	aa					2652

<210> SEQ ID NO 8

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 8

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu	
1																15

Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu	
																20
																25
																30

Ala	Arg	Glu	Gln	Leu	Ala	Leu	Glu	His	Glu	Ser	Tyr	Glu	Met	Gly	Glu	
																35
																40
																45

Ala	Arg	Phe	Arg	Lys	Met	Phe	Glu	Arg	Gln	Leu	Lys	Ala	Gly	Glu	Val	
																50
																55
																60

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys

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65	70	75	80
Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg 85	90	95	
Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu 100	105	110	
Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser 115	120	125	
Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala 130	135	140	
Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys 145	150	155	160
His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His 165	170	175	
Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser 180	185	190	
Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp 195	200	205	
Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr 210	215	220	
Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp 225	230	235	240
Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr 245	250	255	
Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val 260	265	270	
Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Tyr Trp Ala 275	280	285	
Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala 290	295	300	
Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile 305	310	315	320
Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala 325	330	335	
Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile 340	345	350	
Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp 355	360	365	
Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val 370	375	380	
Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe 385	390	395	400
Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe 405	410	415	
Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe 420	425	430	
Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys 435	440	445	
Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly 450	455	460	
Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys 465	470	475	480
Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro 485	490	495	

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Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
 500 505 510
 Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
 515 520 525
 Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
 530 535 540
 His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
 545 550 555 560
 Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
 565 570 575
 Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
 580 585 590
 Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
 595 600 605
 Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
 610 615 620
 Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
 625 630 635 640
 Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln
 645 650 655
 Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Thr Gly Glu Ile Leu Arg
 705 710 715 720
 Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
 725 730 735
 Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
 740 745 750
 Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
 755 760 765
 Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
 770 775 780
 Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
 785 790 795 800
 Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
 805 810 815
 Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
 820 825 830
 Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
 835 840 845
 Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
 850 855 860
 Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
 865 870 875 880
 Ala Phe Ala

<210> SEQ ID NO 9
 <211> LENGTH: 2652
 <212> TYPE: DNA

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<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 9

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ttcaacactc tggctgacca	ttacggtag cgtttagctc gccaacagt ggccctttag	120
catgagtctt acgagatggg	tgaaggcacgc ttccgcaaga tgtttgagcg tcaacttaaa	180
gtcggtgagg ttgcggataa	cgtgccgca aaggctctca tcactaccct actccctaag	240
atgattgcac gcatcaacga	ctggttttag gaagtgaaag ctaagegcgg caagcgccg	300
acagccttcc agttctgca	agaaaatcaag ccggaagccg tagcgtacat caccattaag	360
accactctgg cttgcctaac	cagtgctgac aatacaaccg ttcaaggctgt agcaagcgca	420
atcggtcggg ccattgagga	cgaggctcgc ttccggctgta tccgtgaccc tgaagctaag	480
cacttcaaga aaaacgttga	ggaacaactc aacaagcgcc tagggcacgt ctacaagaaa	540
gcatttatgc aagttgtcga	ggctgacatg ctctctaagg gtctactcgg tggcgaggcg	600
tggcttcgt ggcataagga	agactctatt catgttaggag tacgctgcat cgagatgtc	660
attgagtcaa ccggaatgggt	tagtttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcgc	acctgaatac gctgaggcata tcgcaacccg tgcagggtgc	780
ctggctggca tctctccgat	gttccaaacct tgcgttagttc ctccctaagcc gtggacttgc	840
attactggtg gtggctattt	ggctaacgggt cgtcgcttcc tggcgctggc gctgtactcac	900
agtaagaaag cactgatgcg	ctacgaagac gtttacatgc ctgagggtta caaagcgatt	960
aacattgcgc aaaacaccgc	atggaaaatc aacaagaaag tccttagcggt cgccaaacgta	1020
atcacaagg ggaagcattt	tccggtcgag gacatccctg cgattgagcg tgaagaactc	1080
ccgatgaaac cggaaagacat	cgacatgaat cctgaggctc tcaccgcgtg gaaacgtgct	1140
gccgctgctg tgcgttccaa	ggacaaggct cgcaagtctc gccgtatcag ctttgagttc	1200
atgcgttgcg aagcaataa	gtttgctaac cataaggcca tctgggtccc ttacaacatg	1260
gactggcgcg gtcgttta	cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc	1320
aaaggactgc ttacgttgc	gaaaggtaaa ccaatcggtt aggaagggtt ctactggctg	1380
aaaatccacg gtgcaaaactg	tgcgggtgtc gataaggttc cgttccctga ggcgtatcaag	1440
ttcatttgggg	aaaaccacga gaacatcatg gcttgcgtt agtctccact ggagaacact	1500
tggggctg agcaagattt	tccgttctgc ttcccttgcgt tctgttttgc gtacgcttgc	1560
gtacagcacc acggcgttgc	ctataactgc tcccttccgc tggcggttgc cgggtcttgc	1620
tctggcatcc agcacttctc	cgcgtatgtc cgagatgagg taggtggctc cgccgttaac	1680
ttgtttccat gtgaaaccgt	tcaggacatc tacgggattt ttgttcaagaa agtcaacgag	1740
attctacaag cagacgcaat	caatgggacc gataacgaag tagttaccgt gaccgtatgg	1800
aacactggtg aaatctctga	gaaaggtaag ctgggcacta aggcaactggc tggtcaatgg	1860
ctggcttacg gtgttactcg	cagtgtgact aagcggttgc tcatgacgtt ggcttacggg	1920
tccaaaggat tccggcttccg	tcaacaaggta ctggaaagata ccattcagcc agtattgtat	1980
tccggcaagg gtctgtatgtt	cactcagcc aatcaggctg ctggatacat ggctaaatgt	2040
atttggaaat ctgtgagcgt	gacgggtggta gctgcgggtt aagcaatgaa cgggcttaag	2100
tctgtgttca agctgttgc	tgctgttgcgtt aaagataaga agactggaga gatttttgc	2160
aagcggttgcg ctgtgttgc	ggtaacttgc gatgggttcc ctgtgttgc ggaataacaag	2220
aagccttattc agacgcgtt	gaacctgtatg ttcctcggtc agttccgctt acagcctacc	2280

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attaacacca acaaagatag cgagattgat gcacacaaac aggagtctgg tatcgctcct	2340
aactttgtac acagccaaga cggtagccac ctgcgttaaga ctgttagtgtg ggcacacgag	2400
aagtacggaa tcgaatctt tgcactgatt cacgactcct tcggtaccat tccggctgac	2460
gctgcgaacc tgtaaaagc agtgcgcaaa actatggttg acacatatga gtcttgtgat	2520
gtactggctg atttctacga ccagttcgct gaccagttgc acgagtctca attggacaaa	2580
atgccagcac ttccggctaa aggtaacttg aacctccgtg acatctttaga gtcggacttc	2640
gcttcgcgt aa	2652

<210> SEQ ID NO 10

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 10

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu			
1	5	10	15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu			
20	25	30	

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu			
35	40	45	

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val			
50	55	60	

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys			
65	70	75	80

Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg			
85	90	95	

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu			
100	105	110	

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser			
115	120	125	

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala			
130	135	140	

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys			
145	150	155	160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His			
165	170	175	

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser			
180	185	190	

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp			
195	200	205	

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr			
210	215	220	

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gln Asp			
225	230	235	240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr			
245	250	255	

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val			
260	265	270	

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala			
275	280	285	

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala			
290	295	300	

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Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
 305 310 315 320
 Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 325 330 335
 Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 340 345 350
 Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 355 360 365
 Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
 370 375 380
 Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400
 Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe
 405 410 415
 Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430
 Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445
 Gly Lys Pro Ile Gly Lys Glu Gly Tyr Trp Leu Lys Ile His Gly
 450 455 460
 Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
 465 470 475 480
 Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
 485 490 495
 Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
 500 505 510
 Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
 515 520 525
 Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
 530 535 540
 His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Arg Ala Val Asn
 545 550 555 560
 Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
 565 570 575
 Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
 580 585 590
 Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
 595 600 605
 Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
 610 615 620
 Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
 625 630 635 640
 Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
 645 650 655
 Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
 705 710 715 720

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Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> SEQ ID NO 11

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 11

atgaacacgtaa acatcgctt aacatcgac ttctctgaca tcgaactggc tgctatcccg 60

ttcaaacatctt tggctgacca ttacggtagcg cgttagctc gcgaacagtt ggcccttgag 120

catgagtctt acgagatggg tgaaggcacgc ttccgcaaga tgtttgagcg tcaacttaaa 180

gctggtgagg ttgcggataa cgctgccgaa aagcctctca tcaactaccct actccctaag 240

atgattgcac gcatcaacgat ctgggtttagg gaagtgaaaat ctaaggcgcc caagcgcccg 300

acagccttcc agttcctgca agaaatcaag ccggaaagccg tagcgtacat caccattaag 360

accactctgg cttgcctaact cagtgcgtac aataacaaccg ttcaggctgt agcaagcgca 420

atcggtcggg ccattgagga cgaggctcgat ttcgggtcgta tccgtgaccc tgaagctaa 480

cacttcaaga aaaacgttga ggaacaactc aacaaggcgtagggcacgt ctacaagaaaa 540

gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcgg tggcgaggcg 600

tggcttcgtt ggcataagga agactctatt catgttagggat tacgctgtcat cgagatgttc 660

attgagtcaa ccggaaatggt tagtttacac cgccaaaatg ctggcgtagt aggtcaagac 720

tctgagacta tcgaactcgat acctgtatac gctgaggctt tccgtatccc tgcagggtcg 780

ctggctggca tctctccgat gttccaacct tccgtatccc tccgtatccc gtggactggc 840

attactgggt gtggcttattt ggctaacgggt cgctgttccgt tggcgcttgcgtt gcgtactcac 900

agtaagaaatg cactgtatgcg ctacgtatgcg ttttacatgcg ctgagggtgtt caaaggcgatt 960

aacattgcgc aaaacaccgc atggaaaatc aacaaggaaatg tccgtatccc cgccaaatgtt 1020

atcaccatgtt ggaaggatgg tccgtatccc gacatccctt cgattggcg tgaaggatcc 1080

ccgatgaaatc ccggaaatggat cgacatgtatccgt tccgtatccc gaaacgtgtt 1140

ccggctgtgtt tggatccgtt ggttccgtt ggttccgtt ccgtatccgtt cttgtatccc 1200

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<210> SEQ_ID NO 12
<211> LENGTH: 883
<212> TYPE: PRT
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 12

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
 1 5 10 15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
20 25 30

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
 35 40 45

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
50 55 60

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
65 70 75 80

Met Ile Ala Arg Ile Asp Asp Ile Phe Gln Glu Glu Val Lys Ala Lys Arg
 85 90 95
 Glu Ile Asp Pro Thr Ile Phe Gln Phe Ile Gln Glu Ile Ile Pro Glu

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Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
 115 120 125
 Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
 130 135 140
 Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 145 150 155 160
 His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
 165 170 175
 Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 180 185 190
 Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 195 200 205
 Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 210 215 220
 Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 225 230 235 240
 Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
 245 250 255
 Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
 260 265 270
 Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
 275 280 285
 Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
 290 295 300
 Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
 305 310 315 320
 Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 325 330 335
 Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 340 345 350
 Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 355 360 365
 Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
 370 375 380
 Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400
 Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe
 405 410 415
 Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430
 Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445
 Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
 450 455 460
 Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
 465 470 475 480
 Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
 485 490 495
 Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
 500 505 510
 Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
 515 520 525

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Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
 530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
 545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
 565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
 580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
 595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
 610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
 625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
 645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
 660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
 675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
 690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
 705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp
 725 730 735

Gln Glu Tyr Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
 740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
 755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
 770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
 785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
 805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
 820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
 835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
 850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
 865 870 875 880

Ala Phe Ala

<210> SEQ_ID NO 13

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 13

atgaacacgtaaacatcgctaaagaacgacttctctgaca tcgaaactggctgatcccg 60
 ttcaaacactctggctgacca ttacggtgag cgtttagctc gcgaaacagtt ggcccttgag 120

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catgagtctt acgagatggg tgaagcacgc ttccgcaaga tggttgagcg tcaacttaaa	180
getgggtgagg ttgcggataa cgctgcccgc aagcctctca tcactaccct actccctaag	240
atgattgcac acatcaacga ctggtttagag gaagtgaaag ctaagcgcgg caagcgcgg	300
acagccttcc agttcttgca agaaatcaag ccggaagccg tagcgtacat caccattaag	360
accactctgg cttgcttaac cagtgtcgac aataacaaccg ttcaggctgt agcaagcgc	420
atcgggtggg ccattgagga cgaggctcg ttcgggtcgta tccgtgacct tgaagctaa	480
cacttcaaga aaaacgttga ggaacaactc aacaagcgcg tagggcacgt ctacaagaaa	540
gcatttatgc aagttgtcga ggctgacatg ctctctaaagg gtctactcg tggcgaggcg	600
tggtcttcgt ggcataagga agactctatt catgttaggag tacgctgcat cgagatgctc	660
attgagtcaa cccggatggg tagtttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcg acctgaatac gctgaggcata tcgcaacccg tgcaggtgcg	780
ctggctggca tctctccat gttccaaccc tgcgttagttc ctccctaaagcc gtggactggc	840
attactggtg gtggctattt ggcttaacggg cgtcgctc tggcgctggg gcgtactcac	900
agtaagaaag cactgtgcg ctacgaagac gtttacatgc ctgagggtta caaagcgtt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tccttagggg cgccaaacgta	1020
atcaccaagt ggaaggattt tccgggtcgag gacatccctg cgattgagcg tgaagaactc	1080
ccgatgaaac cggaaagacat cgacatgaat cctgaggcctc tcaccgcgtg gaaacgtgct	1140
gccgctgctg tgtaccgaa ggacaaggct cgcaagtctc gccgtatcag ctttgagg	1200
atgcttgagc aagccaataa gtttgcatac cataaggccg tctgggtccc ttacaacatg	1260
gactggcgcg gtctgttta cgctgtgtca atgatcacc ctgcgggtaa cgatgtacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggtt aggaaggtaa ctactggctg	1380
aaaatccacg gtgcaaaactg tgccgggtgtc gataaggttc cggtccctga ggcgtatca	1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgtta agtctccact ggagaacact	1500
tggggctgct agcaagattt tccgttctgc ttcttgcgt tctgtttga gtacgctggg	1560
gtacagcacc acggcctgag ctataactgc tccctccgc tggcggttga cgggtctgc	1620
tctggcatcc agcaactctc cgcgatgttc cgagatgagg taggtggctcg cgccgttaac	1680
ttgcttccata gtgaaaccgt tcaggacatc tacgggattt ttgctaaagaa agtcaacgag	1740
attctacaag cagacgcaat caatggacc gataacgaa tagttaccgt gaccgtatgag	1800
aacactggtg aaatctctga gaaagtcaag ctgggcacta aggcaactggc tggcaatgg	1860
ctggcttacg gtgttactcg cagttgtact aagcggttcg tcatgacgtt ggcttacggg	1920
tccaaagagt tcggcttccg tcaacaagtg ctggaaagata ccattcagcc agcttattgt	1980
tccggcaagg gtctgtatgtt cactcagccg aatcaggctg ctggatacat ggctaaagct	2040
atttggaaat ctgtgagcgt gacgggtggta gctgccccgg aagcaatgaa ctggcttaag	2100
tctgctgtca agctgttggc tgctgaggcgt aaagataaga agactggaga gattttcgc	2160
aagcggttcg ctgtgcattt ggtaactctt gatggttcc ctgtgtggca ggaataacaag	2220
aagccttattc agacgcgtt gaaacctgtt ttcctcggtc agttccgtt acagcctacc	2280
attaacacca acaaagatag cgagattgtat gcacacaaac aggagtctgg tatcgctcct	2340
aactttgtac acagccaaga cggtagccac cttcgtaaga ctgtgtgtg ggcacacgag	2400
aagtacggaa tcgaatcttt tgcactgatt cacgactctc tccggctgac	2460

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gctgcgaacc	tgttcaaagc	agtgcgcgaa	actatggttg	acacatatga	gtcttgat	2520
gtactggctg	atttctacga	ccagttcgct	gaccagtgc	acgagtctca	attggacaaa	2580
atgccagcac	ttccggctaa	aggtaacttg	aacctccgtg	acatcttaga	gtcggacttc	2640
gcgttcgcgt	aa					2652

<210> SEQ ID NO 14

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 14

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu			
1	5	10	15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu			
20	25	30	

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu			
35	40	45	

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val			
50	55	60	

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys			
65	70	75	80

Met Ile Ala His Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg			
85	90	95	

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu			
100	105	110	

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser			
115	120	125	

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala			
130	135	140	

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys			
145	150	155	160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His			
165	170	175	

Val Tyr Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser			
180	185	190	

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp			
195	200	205	

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr			
210	215	220	

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp			
225	230	235	240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr			
245	250	255	

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val			
260	265	270	

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala			
275	280	285	

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala			
290	295	300	

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile			
305	310	315	320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala			
325	330	335	

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Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe
405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu

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755	760	765	
Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His			
770	775	780	
Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu			
785	790	795	800
Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr			
805	810	815	
Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met			
820	825	830	
Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln			
835	840	845	
Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu			
850	855	860	
Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe			
865	870	875	880

Ala Phe Ala

<210> SEQ ID NO 15

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 15

atgaacacga ttaacatcgc taagaacgac ttctctgaca tcgaaactggc tgctatcccg	60
ttcaacacgt tggctgacca ttacggtag cgtttagctc gcaacagtt ggcccttgag	120
catgagtctt acgagatggg tgaagcacgc ttccgcaaga tggggaggcg tcaacttaaa	180
gctgggtgagg ttgcggataa cgctgccccc aagcctctca tcactaccct actccctaag	240
atgattgcac acatcaacga ctggtttag gaagtgaaag ctaagcgccg caagegcccc	300
acagccttcc agtctctgca agaaaatcaag ccggaaagccg tagcgtacat caccattaag	360
accactctgg cttgccttaac cagtgctgac aataacaacc ttccaggctgt agcaagcgca	420
atcgggtcggg ccattgagga cgaggctcgcc ttccggctgtc tccgtgacct tgaagctaa	480
cacttcaaga aaaacgttga ggaacaactc aacaagcgccg tagggcacgt ctacaagaaa	540
gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcgg tggcgaggcg	600
tggcttcgtt ggcataagga agactctatt catgttaggag tacgctgcat cgagatgtc	660
attgagtcaa ccggaaatggg tagtttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcgc acctgaatac gctgaggctt tgcaccccg tgcagggtgc	780
ctggctggca tctctccgat gttccaaacct tgcgttagttc ctccctaagcc gtggactggc	840
attractgggtt gtggcttattt ggctaacgggtt cgctcgcttc tggcgctgggt gcgtactcac	900
agtaagaaag cactgatgcg ctacgaagac gtttacatgc ctgagggttcaaaagcgatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tccttagcggtt cgccaaacgtt	1020
atcacaaggat ggaaggattt tccggctcgag gacatccctt cgatttagcg tgaagaactc	1080
ccgatgaaac cggaaagacat cgacatgaat cctgaggctt tcaaccggctt gaaacgtgt	1140
cccgctgtgt ttttacccgaa ggacaaggctt cgcaagtctc ggcgtatcag ctttggat	1200
atgcttggcc aagccaataa gtttgcatac cataaggccat tctgggtccc ttacaacatg	1260
gacttggcgcc gtcgtgttttca accgtgttca atgatcaacc cgcaaggtaa cgatgttacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggttta aggaaggtaa ctactggctt	1380

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aaaatccacg	gtgc当地actg	tgc当地gtc	gataaggttc	cgttccctga	gcatcaag	1440
ttcattgagg	aaaaccacga	gaacatcatg	gcttgc当地ta	agtctccact	ggagaacact	1500
tgg当地ggctg	agcaagattc	tccg当地ctc	ttc当地ttcgct	tctg当地ttga	gtacg当地tgg	1560
gtacagcacc	acggc当地tggag	ctataactgc	tcccttccg	tggc当地ttga	cggg当地tctgc	1620
tctggcatcc	agcacttctc	cgc当地atgctc	cgagatgagg	taggtgg当地tcg	cgc当地gttaac	1680
ttgcttctca	gtgaaaccgt	tcaggacatc	tacggg当地tgg	ttgctt当地agaa	agtcaacgag	1740
attctacaag	cagacgcaat	caatgggacc	gataacgaaag	tagttaccgt	gaccgatgag	1800
aacactggta	aatctctg	gaaagtcaag	ctgggcaacta	aggcacttgc	tgg当地catgg	1860
ctggcttacg	gtgttactcg	cagtgtgact	aagcgtttag	tcatgacgct	ggcttacgg	1920
tccaaagagt	tccg当地ttccg	tcaacaagtg	ctggaaaggta	ccattcagcc	agcttattgat	1980
tccggcaagg	gtctgatgtt	cactcagccg	aatcaggctg	ctggatacat	ggctt当地agct	2040
atttggaaat	ctgtgagcgt	gacggg当地tggta	gctgccc当地tgg	aagcaatgaa	ctggctt当地ag	2100
tctgctgctc	agctgctggc	tgctgaggctc	aaagataaga	agactggaga	gattctt当地cg	2160
aagcgttgcg	ctgtgc当地tgg	ggtaacttct	gatggg当地tcc	ctgtglocaltgg	ggaatacaag	2220
aagccttattc	agacglocaltgg	gaacctgatg	ttccctc当地ggc	agttccgctt	acagccttacc	2280
attaacacca	acaaagatag	cgagattgat	gcacacaac	aggagtctgg	tatcgcttcc	2340
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gctgc当地acc	tgttcaaacc	agtgc当地cgaa	actatggg	acacatatga	gtctt当地gtat	2520
gtactggctg	atttctacga	ccagttcgct	gaccagttgc	acgagttctca	attggacaaa	2580
atgccagcac	ttccggctaa	aggtaacttg	aacccccc当地tgg	acatctt当地aga	gtcggactt	2640
gcgttgc当地gt	aa					2652

<210> SEQ_ID NO 16

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 16

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1								5		10			15		

Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu
								20		25			30		

Ala	Arg	Glu	Gln	Leu	Ala	Leu	Glu	His	Glu	Ser	Tyr	Glu	Met	Gly	Glu
								35		40			45		

Ala	Arg	Phe	Arg	Lys	Met	Phe	Glu	Arg	Gln	Leu	Lys	Ala	Gly	Glu	Val
					50		55			60					

Ala	Asp	Asn	Ala	Ala	Lys	Pro	Leu	Ile	Thr	Thr	Leu	Leu	Pro	Lys	
65								70		75			80		

Met	Ile	Ala	His	Ile	Asn	Asp	Trp	Phe	Glu	Glu	Val	Lys	Ala	Lys	Arg
								85		90			95		

Gly	Lys	Arg	Pro	Thr	Ala	Phe	Gln	Phe	Leu	Gln	Glu	Ile	Lys	Pro	Glu
								100		105			110		

Ala	Val	Ala	Tyr	Ile	Thr	Ile	Lys	Thr	Leu	Ala	Cys	Leu	Thr	Ser	
								115		120			125		

Ala	Asp	Asn	Thr	Thr	Val	Gln	Ala	Val	Ala	Ser	Ala	Ile	Gly	Arg	Ala
								130		135			140		

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Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
145 150 155 160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
165 170 175

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Val
370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe
405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys

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565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn 580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys 595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly 610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly 625	630	635
Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln 645	650	655
Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln 660	665	670
Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr 675	680	685
Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys 690	695	700
Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg 705	710	715
Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp 725	730	735
Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu 740	745	750
Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu 755	760	765
Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His 770	775	780
Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu 785	790	795
Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr 805	810	815
Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met 820	825	830
Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln 835	840	845
Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu 850	855	860
Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe 865	870	875
Ala Phe Ala		

<210> SEQ ID NO 17
<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 17

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ttcaaacatc tggctgacca ttacggtag cgtttagctc gegaacagtt ggcccttgag	120
cataggtctt acgagatggg tgaaggacgc ttccgcaga tggggagcg tcaacttaaa	180
gctggtgagg ttgcggataa cgctgccccc aagcctctca tcactaccct actccctaag	240
atattttgcac acatcaacgca ctgggtttag qaaatggaaa ctaaggcgccg caaggccccg	300

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acagccttcc agttcttgca agaaatcaag ccggaaagccg tagcgatcat caccattaa	360
accactctgg ctgttcataac cagtgtgcac aataacaacc ttccaggctgt agcaagcgca	420
atcggtcggg ccattgagga cgaggctcg ttcggtegta tccgtgaccc tgaagctaag	480
cacttcaaga aaaacgttga ggaacaactc aacaagecg tagggcacgt ctacaagaaa	540
gcatttatgc aagtgtcgaa ggctgacatg ctctctaaagg gtctactcg tggcgaggcg	600
tggcttcgtt ggcataagga agactctatt catgttaggg tacgctgcat cgagatgtc	660
attgagtcaa ccggaatggt tagtttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcgc acctgaataac gctgaggctt tgcaccccg tgcagggtcg	780
ctggctggca tctctccgat gttccaaacct tgcgttagtt ctcctaaagcc gtggactggc	840
attactgggt gtggctattt ggctaacggt cgtcgtcctc tggcgcttgtt gcgtactcac	900
agtaagaaag cactgatgcg ctacgaagac gtttacatgc ctgagggtgtt caaagcgatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tccctagcggt cgccaacgta	1020
atcaccaagt ggaaggattt tccgggtcgag gacatccctg cgattgagcg tgaagaactc	1080
ccgatgaaac cggaagacat cgacatgaat cctgaggctt tcacccgcgtt gaaacgtgct	1140
gccgctgctg tgcgttccaa ggacaaggctt cgcaagtctc gccgtatcag ccttgaggtt	1200
atgcttgagc aagccaataa gtttgcataac cataaggcca tctggttccc ttacaacatg	1260
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatgtgacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggtt aggaaggtaa ctactggctg	1380
aaaatccacg gtgcaactg tgccgggtgtc gataaggttt cgttccctga ggcgtatcaag	1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgttca agtctccact ggagaacact	1500
tggtggctg agcaagattt tccgttctgc ttcccttgcgt tctgcttgcgtt gtaacgttgg	1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcggtttttt cgggtcttc	1620
tctggcatcc agcacttctc cgcgatgttc cgagatgagg taggtggctcg cgcggtaac	1680
ttgcttccata gtgaaaccgt tcaggacatc tacgggattt ttgctaagaa agtcaacgag	1740
attctacaag cagacgcaat caatgggacc gataacgaa tagttaccgtt gaccgtatgag	1800
aacactggtaa aaatctctga gaaagtcaag ctgggcacta aggactggc tggtaatgg	1860
ctggcttacg gtgttactcg cagtcgtactt aagcgttcaag tcatgtacgtt ggcttacggg	1920
tccaaagagt tcggcttccg tcaacaactg ctggaaagata ccattcagcc agctattgt	1980
tccggcaagg gtctgtatgtt cactcagccg aatcaggcttgc ctggatacat ggtcaagctg	2040
atttggaaat ctgtgagcgtt gacgggtggta gctgcgggtt aagcaatgaa cgggtttaag	2100
tctgtgtctt agctgtgtgc tgcgtggatc aaagataaga agactggaga gatttttcgc	2160
aagcgttgcgtt ctgtgcattt ggttaactcctt gatggttcc ctgtgtggca ggaataacaag	2220
aaggccttacg agacgcgtttaa gaaacctgttgc ttccctcggtt agttccgtt acagectacc	2280
attaacacca acaaagatag cgagattgtt gacacacaac aggactggc tatcgcttcc	2340
aactttgtac acagccaaaga cggtagccac ctgcgttcaagat ctgtgtgtt ggcacacgag	2400
aagtacggaa tcgaatcttt tgcactgtt caccgttccat tccggctgac	2460
gtcgcaacc tggtaaaatc agtgcgcgaa actatggttt acacatatga gtcttgcgtt	2520
gtactggctt atttctacga ccaggctgtt gaccgttgc acgagtctca attggacaaa	2580
atgcccacac ttccggctaa aggttaacttgc aacctccgtt acatcttgcgtt gtcggacttc	2640
gcgttgcgtt aa	2652

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<210> SEQ_ID NO 18
<211> LENGTH: 883
<212> TYPE: PRT
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 18

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Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
1           5          10          15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
20          25          30

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
35          40          45

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
50          55          60

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
65          70          75          80

Met Ile Ala His Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
85          90          95

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
100         105         110

Ala Val Ala Tyr Ile Thr Ile Lys Thr Leu Ala Cys Leu Thr Ser
115         120         125

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
130         135         140

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
145         150         155         160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
165         170         175

Val Tyr Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
180         185         190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
195         200         205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
210         215         220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
225         230         235         240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
245         250         255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
260         265         270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
275         280         285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
290         295         300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
305         310         315         320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
325         330         335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
340         345         350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
355         360         365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Val

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89**90**

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370	375	380
Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe		
385	390	395
400		
Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe		
405	410	415
Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe		
420	425	430
Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys		
435	440	445
Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly		
450	455	460
Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys		
465	470	475
480		
Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro		
485	490	495
Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu		
500	505	510
Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr		
515	520	525
Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln		
530	535	540
His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn		
545	550	555
560		
Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys		
565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn		
580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys		
595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly		
610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly		
625	630	635
640		
Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln		
645	650	655
Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln		
660	665	670
Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr		
675	680	685
Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys		
690	695	700
Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg		
705	710	715
720		
Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp		
725	730	735
Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu		
740	745	750
Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu		
755	760	765
Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His		
770	775	780
Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu		
785	790	795
800		

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Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> SEQ_ID NO 19

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 19

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ttcaacactc tggctgacca ttacggtag cgtttagctc gccaacagg ggccctttag	120
catgagtctt acgagatggg tgaagcacgc ttccgcaaga tgtttgagcg tcaacttaaa	180
gtctggtaggg ttgcggataa cgctgcccgc aagcctctca tcactaccct actccctaag	240
atgattgcac acatcaacgca ctgggtttag gaagtgaaa ctaaggcgcc caagcgccc	300
acagccttcc agttccctgca agaaatcaag ccggaagccg tagcgtacat caccattaag	360
accactctgg cttgcctaac cagtgctgac aatacaaccg ttcaggctgt agcaagcgca	420
atcgggtcgcc ccatttaggaa cgaggctcgc ttccggctgta tccgtgaccc tgaagcttaag	480
cacttcaaga aaaacgttga ggaacaactc aacaaggcg tagggcacgt ctacaagaaa	540
gcattttatgc aagtttcgca ggctgacatg ctctctaagg gtctactcggttggcgaggcg	600
tggcttcgtt ggcataagga agactctatt catgttaggaa tacgctgtcat cgagatgctc	660
attgagtcaa ccggaaatggg tagtttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcgc acctgaatac gctgaggctt tgcaccccg tgcagggtcg	780
ctggctggca tctctccgat gttccaaacct tgcgttagttt ctcctaaagcc gtggactggc	840
attactggtg gtggctattt ggcttaacggc cgtcgctctc tggcgctgtt gcgtactcac	900
agtaagaaag cactgtatgc ctacaaagac gtttacatgc ctgagggttta caaaggcatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tccctagggctt cgccaaacgta	1020
atcaccaagt ggaaggattt tccggctcgag gacatccctc cgatttagcg tgaagaactc	1080
ccgatgaaac cggaaagacat cgacatgaat cctgaggctt tcaccggctt gaaacgtgt	1140
ggcgctgtctg ttttccggca ggacaaaggctt cgcaagtcttccgcgtttagtttcc	1200
atgcttgcgc aagccaataa gtttgcatac cataaggccca tctgggttccc ttacaacatg	1260
gactggcgcc gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggttta aggaagggttta ctactggctg	1380
aaaatccacg gtgcaactg tgcgggtgtc gataaggttt cgttccctga ggcgtatcaag	1440
ttcattggggaaaaccacga gaacatcatg gcttgcgttca agtctccact ggagaacact	1500
tggtggctg agcaagattt tccgttctgc ttcccttgcgt tctgctttga gtacgctggg	1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcggttga cgggtctgc	1620

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tctggcatcc	agcacttctc	cgcgtatgctc	cgagatgagg	taggtggtcg	cgcggtaac	1680
ttgcgttcta	gtgaaaccgt	tcaggacatc	tacgggattg	ttgctaaagaa	agtcaacgag	1740
attctacaag	cagacgcaat	caatgggacc	gataacgaag	tagttaccgt	gaccgtatgag	1800
aacactggtg	aatctctga	gaaagtcaag	ctggggacta	aggcactggc	tggtcaatgg	1860
ctggcttacg	gtgttactcg	cagtgtgact	aagcggttcag	tcatgacgct	ggcttacggg	1920
tccaaagagt	tcgggttccg	tcaacaagtg	ctggaaagata	ccattcagcc	agcttattgat	1980
tccggcaagg	gtctgtatgtt	cactcagccg	aatcaggctg	ctggatacat	ggctaagctg	2040
atttggaaat	ctgtgagcgt	gacgggtgta	gctgcggttg	aagcaatgaa	ctggcttaag	2100
tctgctgcta	agctgctggc	tgctgaggc	aaagataaga	agactggaga	gattcttcgc	2160
aagcggttcg	ctgtgcattt	ggtaactcct	gatggttcc	ctatgtggca	ggaataacaag	2220
aaggcctattc	agacgcgc	tttgcattt	gaacctgtat	ttcctcggtc	agttccgc	2280
attaacacca	acaaagatag	cgagattgtat	gcacacaaac	aggagtctgg	tatcgctcct	2340
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aagtacggaa	tcaaatcttt	tgcactgatt	cacgactc	tccggat	tccggctgac	2460
gtgtgcgaacc	tgttcaaagc	agtgcgcgaa	actatggttg	acacatatga	gtcttgat	2520
gtactggctg	atttctacga	ccagttcgct	gaccgttgc	acgagtctca	attggacaaa	2580
atgccagcac	ttccggctaa	aggtaacttg	aacctccgt	acatctttaga	gtcggacttc	2640
gcgttgcgt	aa					2652

<210> SEQ ID NO 20

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 20

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1				5			10						15		

Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu
		20					25					30			

Ala	Arg	Glu	Gln	Leu	Ala	Leu	Glu	His	Glu	Ser	Tyr	Glu	Met	Gly	Glu
	35				40				45						

Ala	Arg	Phe	Arg	Lys	Met	Phe	Glu	Arg	Gln	Leu	Lys	Ala	Gly	Glu	Val
	50				55				60						

Ala	Asp	Asn	Ala	Ala	Lys	Pro	Leu	Ile	Thr	Thr	Leu	Leu	Pro	Lys	
65					70			75			80				

Met	Ile	Ala	His	Ile	Asn	Asp	Trp	Phe	Glu	Glu	Val	Lys	Ala	Lys	Arg
	85				90				95						

Gly	Lys	Arg	Pro	Thr	Ala	Phe	Gln	Phe	Leu	Gln	Glu	Ile	Lys	Pro	Glu
	100				105			110							

Ala	Val	Ala	Tyr	Ile	Thr	Ile	Lys	Thr	Leu	Ala	Cys	Leu	Thr	Ser	
	115				120			125							

Ala	Asp	Asn	Thr	Thr	Val	Gln	Ala	Val	Ala	Ser	Ala	Ile	Gly	Arg	Ala
130					135			140							

Ile	Glu	Asp	Glu	Ala	Arg	Phe	Gly	Arg	Ile	Arg	Asp	Leu	Glu	Ala	Lys
145					150			155			160				

His	Phe	Lys	Lys	Asn	Val	Glu	Glu	Gln	Leu	Asn	Lys	Arg	Val	Gly	His
	165				170			175							

Val	Tyr	Lys	Lys	Ala	Phe	Met	Gln	Val	Val	Glu	Ala	Asp	Met	Leu	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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180	185	190
Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp		
195	200	205
Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr		
210	215	220
Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp		
225	230	235
240		
Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr		
245	250	255
Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val		
260	265	270
Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala		
275	280	285
Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala		
290	295	300
Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile		
305	310	315
320		
Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala		
325	330	335
Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile		
340	345	350
Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp		
355	360	365
Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val		
370	375	380
Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe		
385	390	395
400		
Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe		
405	410	415
Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe		
420	425	430
Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys		
435	440	445
Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly		
450	455	460
Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys		
465	470	475
480		
Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro		
485	490	495
Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu		
500	505	510
Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr		
515	520	525
Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln		
530	535	540
His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn		
545	550	555
560		
Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys		
565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn		
580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys		
595	600	605

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Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> SEQ ID NO 21

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 21

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ttcaacactc tggctgacca ttacggtag cgtttagctc gccaacagtt ggcccttgag	120
catgagtctt acgagatggg tgaagcacgc ttccgcaaga tgttttagcg tcaacttaaa	180
gttgttggagg ttgcggataa cgctgccgcc aagcctctca tcactaccct actccctaag	240
atgattgcac gcatcaacga ctggttttag gaagtgaaag ctaagcgccg caagcgcccg	300
acagccttcc agttcctgca agaaatcaag ccgaaagccg tagcgtacat caccattaag	360
accactctgg cttgcctaac cagtgcgtac aataacaacc ttccaggctgt agcaagcgca	420
atcggctggg ccattgagga cgaggctcgc ttccgtcgta tccgtgactt tgaagctaa	480
cacttcaaga aaaacgttga ggaacaactc aacaagcgccg tagggcacgt ctacaagaaa	540

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gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcg tggcgaggcg	600
tggcttcgt ggcataagga agactctatt cattaggag tacgctgcgt cgagatgtc	660
attgagtcaa ccggaatggt tagtttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcgc acctgaatac gctgaggcta tgcacaaccg tgcaggtgcg	780
ctggctggca tctctccgt gttccaacct tgcgttagttc ctccataagcc gtggactggc	840
attactggtg gtggcttattg ggctaacggc cgtcgcttc tggcgcttgtt gcgtactcac	900
agtaagaaag cactgatgcg ctacgaagac gtttacatgc ctgagggtta caaagcgatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tccctagcggt cgccaaacgta	1020
atcaccaagt ggaagcatttgc tccggcgtc gacatccctg cgattgagcg tgaagaactc	1080
cggatgaaac cggaaagacat cgacatgaat cctgaggcgc tcaccggcgt gaaacgtgct	1140
gecgctgctg tgtaccgcaa ggacaaggctt cgcgtatcgttgc ccttgaggttc	1200
atgcgttgagc aagccaataa gtttgcatac cataaggccg tctgggtccc ttacaacatg	1260
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggttta aggaaggtaa ctactggctg	1380
aaaatccacg gtgcacactg tgccgggtgtc gataaggttc cggtccctgac ggcacatcaag	1440
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tggggctg agcaagatttgc tccgttctgc ttccctggcgt tctgcttgcgttgc	1560
gtacagcacc acggcctgag ctataactgc tccctccgc tggcggttgc cgggtctgc	1620
tctggcatcc agcaacttctc cgcgtatgc cggatgagg taggtggcgt cgggttaac	1680
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attctacaag cagacgcaat caatgggacc gataacgaag tagttaccgt gaccgtatgg	1800
aacactggtaa aatctctga gaaaggtaa ctgggcacta aggcaactggc tggtaatgg	1860
ctggcttacg gtgttactcg cagtgactt aagcggttacg tcatgacgct ggcttacggg	1920
tccaaagagt tcgggttccg tcaacaagtg ctggaaaggta ccattcagcc agtatttgat	1980
tccggcaagg gtctgtatgtt cactcagccg aatcaggctg ctggatacat ggctaaagctg	2040
atttggaaat ctgtgagcgt gacgggttgc gctgggttgc aagcaatgaa ctgggtttaag	2100
tctgctgtca agctgctggc tgctgaggcgtt aaagataaga agactggaga gattttcgc	2160
aagcgttgcg ctgtgttgcgtt ggttaacttgcgtt gatggtttgc tctgtgttgc ggaatacaag	2220
aagcctatttca agacgcgtt gaaacctgtt gttccctggcgtt agttcccgctt acagcctacc	2280
attaacacca acaaagatag cgagattgtt gacacacaac aggagtctgg tatacgcttcc	2340
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gctgcgaacc tggtaaaagc agtgcgcgaa actatgggttgc acacatatgaa gtcttgcgtt	2520
gtactggctg atttctacgtt ccagttcgctt gaccagggttgc acgagtctca attggacaaa	2580
atgccagcac ttccggctaa aggttaacttgc aacccctccgtt acatcttgcgtt gtcggacttc	2640
gggttcgttgcgtt aa	2652

<210> SEQ ID NO 22

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

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101**102**

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<400> SEQUENCE: 22

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
 1 5 10 15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
 20 25 30

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
 35 40 45

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
 50 55 60

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
 65 70 75 80

Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
 85 90 95

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
 100 105 110

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
 115 120 125

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
 130 135 140

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 145 150 155 160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
 165 170 175

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
 245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
 260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Tyr Trp Ala
 275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
 290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
 305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Val
 370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe
 405 410 415

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Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430
 Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445
 Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
 450 455 460
 Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
 465 470 475 480
 Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
 485 490 495
 Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
 500 505 510
 Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
 515 520 525
 Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
 530 535 540
 His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
 545 550 555 560
 Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
 565 570 575
 Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
 580 585 590
 Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
 595 600 605
 Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
 610 615 620
 Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
 625 630 635 640
 Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln
 645 650 655
 Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
 705 710 715 720
 Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
 725 730 735
 Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
 740 745 750
 Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
 755 760 765
 Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
 770 775 780
 Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
 785 790 795 800
 Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
 805 810 815
 Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
 820 825 830

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Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val	Leu	Ala	Asp	Phe	Tyr	Asp	Gln
								835				840			845

Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln	Leu	Asp	Lys	Met	Pro	Ala	Leu
						850		855			860				

Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg	Asp	Ile	Leu	Glu	Ser	Asp	Phe
		865		870				875				880			

Ala Phe Ala

<210> SEQ ID NO 23

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 23

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catgagtctt	acgagatggg	tgaaggcacgc	ttccgcaaga	tgtttgagcg	tcaacttaaa	180
gttgtgagg	ttgcggataa	cgcgtccgccc	aagcctctca	tcactaccct	actccctaag	240
atgattgcac	gcatcaacgca	ctgggtttag	gaagtgaaa	ctaagcgccg	caagcgcccc	300
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accactctgg	ttgctctaac	cagtgtac	aatacaacc	ttcaggctgt	agcaagcgca	420
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cacttcaaga	aaaacgttga	ggaacaactc	aacaagcg	tagggcacgt	ctacaagaaaa	540
gcatttatgc	aagttgtcga	ggctgacatg	ctctctaagg	gtctactcg	tggcgaggcg	600
tggcttcgt	ggcataagga	agactctatt	catgttaggg	tacgctgcat	cgagatgtc	660
attgagtcaa	ccggaatgg	tagttacac	cgcacaaatg	ctggcgtagt	aggtaagac	720
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ccgatgaaac	cggaagacat	cgacatgaat	cctgaggctc	tcacccgcgt	gaaacgtgct	1140
gccgctgctg	tgtaccgcaa	ggacaaggct	cgcaagtctc	gccgtatcag	ccttgagttc	1200
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attaacacca acaaagatag cgagattgat gcacacaaac aggagtctgg tatcgctcct 2340
aactttgtac acagccaaga cggtagccac cttcgtaa ctgttagtgg ggcacacgag 2400
aagtacggaa tcgaatctt tgcactgatt cacgactcct tcggtaaccat tccggctgac 2460
gctgcgaacc tgttcaaagc agtgcgcgaa actatggttt acacatatga gtcttgtat 2520
gtactggctg atttctacga ccagttcgctt gaccagtgc acgagtctca attggacaaa 2580
atgccagcac ttccggctaa aggttaacttg aacctccgtg acatctttaga gtcggacttc 2640
gcgttcgcgt aa 2652

```

<210> SEQ_ID NO 24

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 24

```

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
1 5 10 15

```

```

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
20 25 30

```

```

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
35 40 45

```

```

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
50 55 60

```

```

Ala Asp Asn Ala Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
65 70 75 80

```

```

Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
85 90 95

```

```

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
100 105 110

```

```

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
115 120 125

```

```

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
130 135 140

```

```

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
145 150 155 160

```

```

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
165 170 175

```

```

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
180 185 190

```

```

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
195 200 205

```

```

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
210 215 220

```

-continued

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe
405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

-continued

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
 645 650 655
 Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
 705 710 715 720
 Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
 725 730 735
 Gln Glu Tyr Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
 740 745 750
 Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
 755 760 765
 Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
 770 775 780
 Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
 785 790 795 800
 Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
 805 810 815
 Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
 820 825 830
 Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
 835 840 845
 Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
 850 855 860
 Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
 865 870 875 880
 Ala Phe Ala

<210> SEQ ID NO 25
 <211> LENGTH: 2652
 <212> TYPE: DNA
 <213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 25

```

atgaacacgtaaacatcgcttaagaacgacttctctgaca tgcgaaactggctgttatcccg 60
ttcaacactctggctgacca ttacggtagcgtttagctc gcgaaacagtt ggcccttgag 120
catgagtcttacgagatgggtgaaggcacgc ttccgcaga tggtagcgctcaacttaaa 180
gttggtaggg ttgcggataa cgctgccc aagccttcataactaccct actccctaa 240
atgattgcac gcatcaacgacttgcgtttagaa gaaatgaaacttgcgaaacggcc 300
acagccttcc agttcctgca agaaatcaag cccggaaagccg tagcgtacat caccattaag 360
accactctgg ctgccttaac cagtgctgac aatacaaccg ttcaggctgt agcaagcgca 420
atcggttgcggccatgttggaa cgaggctcgcttcggctgtaccc tggtagctaa 480
cacttcaaga aaaacgttga ggaacaactc aacaaggcgtagggcacgt ctacaagaaa 540
gcattttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcgg tggcgaggcg 600
tggtcttcgttggcataagga agactctatt catgttaggat tacgctgcat cgagatgctc 660
atggagtcaa ccggaatggtagcttacac cgccaaaatgc tggcgttagt aggtcaagac 720
  
```

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tctgagacta tcgaactcgc acctgaatac gctgaggcta tcgcaacccg tgcaggtgcg	780
ctggctggca tctctccgat gttccaacct tgctgtatcc tccttaagcc gtggactggc	840
attactggtg gtggatattg ggctaacggt cgtcgtctc tggcgcttgt gcgtactcac	900
agtaagaag cactgatgcg ctacaaagac gtttacatgc ctgagggtgt caaagcgatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaag tcctagcggt cgccaaacgta	1020
atcacaagg ggaaggattg tccggctcgag gacatccctg cgattgagcg tgaagaactc	1080
ccgatgaaac cggaaagacat cgacatgaat cctgaggctc tcaccgcgtg gaaacgtgct	1140
gccgctgctg tgtaccgaa ggacaaggct cgcaagtctc gccgtatcag ccttgagttc	1200
atgcttgagc aagccaataa gtttgcatac cataaggccg tctggttccc ttacaacatg	1260
gactggcgcg gtcgtgtta cgctgtgtca atgatcacc cgcaaggtaa cgatatgacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggttta aggaaggtaa ctactggctg	1380
aaaatccacg gtgcaaactg tgccgggtgtc gataaggttc cgttccctga ggcgcataag	1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgtca agtctccact ggagaacact	1500
tgggtggctg agcaagattc tccgttctgc ttccctgtcg tctgcttgcgt gtacgctggg	1560
gtacagcacc acggcctgag ctataactgc tcccttcgc tggcggttgc cgggtctgc	1620
tctggcatcc agcacttctc cgcgatgctc cgagatgagg taggtggctcg cgccgttaac	1680
ttgcttccta gtgaaaccgt tcaggacatc tacgggatgtt ttgctaaagaa agtcaacgag	1740
attctacaag cagacgcaat caatgggacc gataacgaag tagttaccgt gaccgatgag	1800
aacactggtaa aatctctga gaaagtcaag ctgggcacta aggcaactggc tggtaatgg	1860
ctggcttacg gtgttactcg cagtgact aagcggttgc tcatgacgct ggcttacggg	1920
tccaaagagt tccggcttccg tcaacaagtgc ctggaaagata ccattcagcc agctattgtat	1980
tccggcaagg gtctgtgtt cactcagccg aatcaggctg ctggatacat ggctaaagctg	2040
atttggaaat ctgtgagcgt gacgggtggta gctgcgggttgc aagcaatgaa ctggcttaag	2100
tctgctgtca agctgtggc tgctgaggctc aaagataaga agactggaga gattcttcgc	2160
aagcggtcgctg ctgtgcattt ggttaactctt gatggttcc ctatgtggca ggaataacaag	2220
aaggcttattc agacgcgtt gaaacctgtat ttcctcggtc agttccgtt acaggcttacc	2280
attaacacca acaaagatag cgagattgtat gcacacaaac aggagtctgg tatcgctcct	2340
aactttgtac acagccaaga cggtagccac cttcgtaaga ctgtgtgttgc ggcacacgag	2400
aagtagcggaa tcaaatcttt tgcaactgatt cacgactctc tccggatccat tccggctgac	2460
gtgtcgaaacc tggtaaaaggc agtgcgcgaa actatggtttgc acacatatgaa gtcttgcgt	2520
gtactggctg atttctacga ccaggctcgtt gaccaggcttgc acaggatctca attggacaaa	2580
atggccagcac ttccggctaa aggttaacttgc aacccctcggttgc acatcttgcgttgc gtcggacttc	2640
gggttcggctgtt aa	2652

<210> SEQ ID NO 26

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 26

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1															

5 10 15

Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu
20															

25 30

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Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
 35 40 45

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
 50 55 60

Ala Asp Asn Ala Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
 65 70 75 80

Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
 85 90 95

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
 100 105 110

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
 115 120 125

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
 130 135 140

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 145 150 155 160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
 165 170 175

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
 245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
 260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
 275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
 290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
 305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Val
 370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe
 405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445

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Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe

-continued

865

870

875

880

Ala Phe Ala

<210> SEQ ID NO 27
<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 27

atgaacacga ttaacatcg	taagaacgac ttctctgaca	tcgaactggc tgctatccg	60
ttcaacac	tggctgacca ttacggtag	cgttagctc gcaacagt ggccctttag	120
catgagtctt acgagatggg tgaagcacgc ttccgcaaga tgtttgagcg tcaacttaaa	180		
gctggtaggg ttgcggataa cgctgccgc aagcctctca tcactaccct actccctaag	240		
atgattgcac gcatcaacga ctggtttag gaagtgaaag ctaagcgccg caagcgccg	300		
acagccttcc agttcctgca agaaatcaag ccggaagccg tagcgtacat caccattaag	360		
accactctgg cttgcctaact cagtgcgtac aataacaacc ttcaaggctgt agcaagcgca	420		
atcggctggg ccatttaggga cgaggctcg ttcggctgta tccgtgacct tgaagctaag	480		
cacttcaaga aaaacgttga ggaacaactc aacaagcgccg tagggcacgt ctacaagaaa	540		
gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcgg tggcgaggcg	600		
tggcttcgtt ggcataagga agactctatt catgttaggag tacgctgcat cgagatgtc	660		
attgagtcaa ccggaatggg tagttacac cgccaaaatg ctggcgtagt aggtcaagac	720		
tctgagacta tcgaactcgc acctgaatac gctgaggcta tcgcaaccgc tgcaggtgcg	780		
ctggctggca tctctccgat gttccaacct tgcgttagttc ctccctaagcc gtggactggc	840		
attactggtg gtggcttattt ggctaacggcg cgctcgctc tggcgctgtt gcgtactcac	900		
agtaagaaag cactgatgcg ctacgaagac gtttacatgc ctgaggtgta caaagcgatt	960		
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tcctagcggt cgccaaacgta	1020		
atcacaagt ggaagcattt tccggctcgag gacatccctg cgattgagcg tgaagaactc	1080		
ccgatgaaac cggaaagacat cgacatgaat cctgaggctc tcaccgcgtg gaaacgtgct	1140		
gccgctgctg tgtaccgcaa ggacaaggct cgcaagtctc gccgtatcag ctttgagttc	1200		
atgcttgagc aagccaataa gtttgcatac cataaggcca tctgggtccc ttacaacatg	1260		
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc	1320		
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggtt aggaagggtt ctactggctg	1380		
aaaatccacg gtgcaaactg tgccgggtgctc gataaggttc cgttccctga ggcgcataag	1440		
ttcattgagg aaaaccacga gaacatcatg gcttgcgtca agtctccact ggagaacact	1500		
tggggctg agcaagattt tccgttctgc ttcccttgcgt tctgctttga gtacgctggg	1560		
gtacagcacc acggccctgag ctataactgc tccctccgc tggcggttga cgggtctgc	1620		
tctggcatcc agcaacttctc cgcgatgtc cgagatgagg taggtggctcg cgccgttaac	1680		
ttgcttccta gtgaaaccgt tcaggacatc tacgggatgg ttgctaaagaa agtcaacgag	1740		
attctacaag cagacgcaat caatgggacc gataacgaag tagttaccgt gaccgatgag	1800		
aacactggtg aaatctctga gaaagtcaag ctgggcacta aggcaactggc tggtaatgg	1860		
ctggcttacg gtgttactcg cagtgtgact aagcgttcg tcatgacgt ggcttacggg	1920		
tccaaagagt tcggcttccg tcaacaagtg ctggaaaggtt ccattcagcc agctatttgat	1980		
tccggcaagg gtctgtatgtt cactcagccg aatcaggctg ctggatacat ggctaaatcg	2040		

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atttggaaat ctgtgagcgt gacggtggt a gctgcggttg a a gcaatgaa cgggcttaag 2100
tctgctgcta agctgctggc t gctgaggtc aa agataaga a gactggaga gattttcg 2160
a a g c g t t g c g ctgtgcattt g gtaactctt gatggttcc ctgtgtggca ggaatacaag 2220
a a g c c t a t t c a g a c g c g t t g a a c c t g a t g t t c g g c t t a c c 2280
a t t a a c a c c a a c a a a g a t a g c g a t t g a t t g a t t g a t t g a t t 2340
a a c t t t g t a c a c a a g a c g g a a c g g a c a c g a g a c a c g a g 2400
a a g t a c g g a a t c g a a t c t t t g c a c t g a t t c a c g a c t c t t 2460
g e t g c g a a c c t g t c a a a g c t g c g a a c t a t g g t t g a c a c a t a t g a 2520
g t a c t g g c t g a t t t c t a c g a c c a g t t c g t g a c g a g t c t c a 2580
a t g c c a g c a c t t c g g c t a a a g g t a a c t t g a a c a t c t t a g a 2640
g c g t t c g c g t a a 2652

```

<210> SEQ ID NO 28

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 28

```

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
1 5 10 15

```

```

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
20 25 30

```

```

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
35 40 45

```

```

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
50 55 60

```

```

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
65 70 75 80

```

```

Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
85 90 95

```

```

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
100 105 110

```

```

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
115 120 125

```

```

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
130 135 140

```

```

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
145 150 155 160

```

```

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
165 170 175

```

```

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
180 185 190

```

```

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
195 200 205

```

```

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
210 215 220

```

```

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
225 230 235 240

```

```

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
245 250 255

```

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Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Val
370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe
405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr

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675	680	685
Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys		
690	695	700
Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg		
705	710	715
720		
Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp		
725	730	735
Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu		
740	745	750
Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu		
755	760	765
Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His		
770	775	780
Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu		
785	790	795
800		
Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr		
805	810	815
Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met		
820	825	830
Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln		
835	840	845
Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu		
850	855	860
Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe		
865	870	875
880		
Ala Phe Ala		

<210> SEQ_ID NO 29
<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

-continued

aacattgcgc	aaaacaccgc	atggaaaatc	aacaagaaag	tccttagcggt	cggcaacgta	1020
atcaccaagt	ggaagcattt	tccggtcgag	gacatccctg	cgattgagcg	tgaagaactc	1080
ccgatgaaac	cggaagacat	cgacatgaat	cctgaggctc	tcaccgcgtg	gaaacgtgct	1140
gccgctgctg	tgtaccgcaa	ggacaaggct	cgcaagtctc	gccgttatcag	ccttgagttc	1200
atgcgttgc	aagccaataa	gtttgctaac	cataaggcca	tctggttccc	ttacaacatg	1260
gactggcg	gtcggttta	cgtcggtca	atgttcaacc	cgcaaggtaa	cgatgtgacc	1320
aaaggactgc	ttacgctggc	gaaaggtaaa	ccaatcggtt	aggaaggta	ctactggctg	1380
aaaatccacg	gtgcaaactg	tgcgggtgtc	gataaggttc	cgttccctga	gccccatcaag	1440
ttcattgagg	aaaaccacga	gaacatcatg	gcttgcgcta	agtctccact	ggagaacact	1500
tggggctg	agcaagattc	tccgttctgc	tcccttgcgt	tctgcttga	gtacgctggg	1560
gtacagcacc	acggcctgag	ctataactgc	tcccttccgc	tggcggttga	cgggtcttgc	1620
tctggcatcc	agcacttctc	cgcgtatctc	cgagatgagg	taggtggctg	cgcggtaaac	1680
ttgcttca	gtgaaaccgt	tcaggacatc	tacgggattt	ttgctaagaa	agtcaacgag	1740
attctacaag	cagacgcaat	caatggacc	gataacgaag	tagttaccgt	gaccgtatgag	1800
aacactgg	aaatctctga	gaaagtcaag	ctgggcacta	aggcactggc	tggtaatgg	1860
ctggcttacg	gtgttactcg	cagtgtgact	aagcgttca	tcatgacgct	ggcttacggg	1920
tccaaagagt	tcggettcg	tcaacaagt	ctggaaaggta	ccattcagcc	agctatttgat	1980
tccggcaagg	gtctgtatgtt	cactcagccg	aatcaggctg	ctggatacat	ggctaagctg	2040
atttggaaat	ctgtgagcgt	gacgggtggta	gctgcgggtt	aagcaatgaa	ctggettaag	2100
tctgctgct	agctgtctggc	tgtcgaggct	aaagataaga	agactggaga	gattcttgc	2160
aagcggtgc	ctgtgcattt	ggtaactctt	gatggttcc	ctatgtggc	ggaataacaag	2220
aaggcttattc	acacgcgc	tttgcatttgc	agttccgc	acagectacc		2280
attaacacca	acaaagatag	cgagattgt	gcacacaaac	aggagtctgg	tatcgctcct	2340
aactttgtac	acagccaa	cggttagcc	cttcgttgc	ctgtgtgt	ggcacacgag	2400
aagtaeggaa	tcaatcttt	tgcactgatt	cacgactct	tccgttaccat	tccggctgac	2460
gtgtgcgaacc	tgttcaagc	agtgcgcgaa	actatggttt	acacatatga	gtcttgat	2520
gtactggctg	atttctacga	ccagttcgct	gaccagttgc	acgagtctca	attggacaaa	2580
atgccagcac	ttccggctaa	aggtaactt	aaccccggtt	acatcttgc	gtcgacttc	2640
gcgttcgcgt	aa					2652

<210> SEQ ID NO 30

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 30

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1															

5 10 15

Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu
20															

25 30

Ala	Arg	Glu	Gln	Leu	Ala	Leu	Glu	Ser	Tyr	Glu	Met	Gly	Glu	
35														

35 40 45

Ala	Arg	Phe	Arg	Lys	Met	Phe	Glu	Arg	Gln	Leu	Lys	Ala	Gly	Glu	Val
50															

50 55 60

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Ala Asp Asn Ala Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
 65 70 75 80

Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
 85 90 95

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
 100 105 110

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
 115 120 125

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
 130 135 140

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 145 150 155 160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
 165 170 175

Val Tyr Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
 245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
 260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
 275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
 290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
 305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
 370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe
 405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Trp Leu Lys Ile His Gly
 450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
 465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro

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132

485	490	495
Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu		
500	505	510
Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr		
515	520	525
Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln		
530	535	540
His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn		
545	550	555
560		
Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys		
565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn		
580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys		
595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly		
610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly		
625	630	635
640		
Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln		
645	650	655
Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln		
660	665	670
Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr		
675	680	685
Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys		
690	695	700
Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg		
705	710	715
720		
Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp		
725	730	735
Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu		
740	745	750
Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu		
755	760	765
Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His		
770	775	780
Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu		
785	790	795
800		
Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr		
805	810	815
Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met		
820	825	830
Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln		
835	840	845
Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu		
850	855	860
Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe		
865	870	875
880		
Ala Phe Ala		

<210> SEQ ID NO 31
<211> LENGTH: 2652

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<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 31

atgaacacgca ttaacatcgc taagaacgac ttctctgaca tcgaactggc tgctatcccg
ttcaaacactc tggctgacca ttacggtag cgtttagetc gegaacagtt ggcccttgag 1200
catgagtctt acgagatggg tgaagcacgc ttccgcaaga tgtttggcg tcaactaaa 1800
gtggtgagg ttgcggataa cgctgccgc aagcctctca tcaactaccct actccctaag 2400
atgattgcac gcatcaacga ctgggttag gaagtggaa ctaagcgcgg caagcgcgg 3000
acagccttc agttctgca agaaatcaag ccggaaagccg tagcgtacat caccattaag 3600
accactctgg ctgecttaac cagtgtcgac aatacaaccg ttccaggctgt agcaagcgc 4200
atcggtcggg ccattgagga cgaggctcgc ttccggtcgta tccgtgaccc tgaagctaag 4800
cacttcaaga aaaacgttga ggaacaactc aacaaggcgc tagggcacgt ctacaagaaa 5400
gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcg tggcgaggcg 6000
tggcttcgtt ggcataagga agactctatt catgttaggg tacgctgcat cgagatgctc 6600
attgagtcaa ccggaatgg tagttacac cgccaaatg ctggcgtagt aggtcaagac 7200
tctgagacta tcgaactcgc acctgaatac gctgaggcgt tcgcaaccgc tgcaggcgc 7800
ctggctggca tctctccgtt gttcaacct tgctgtttc ctccataagcc gtggactggc 8400
attactgggt gtggcttattt ggctaacggc cgtcgcttc tggcgctgg gcgtactcac 9000
agtaagaaag cactgatgcg ctacgaagac gtttacatgc ctgagggtgtt caaagcgtt 9600
aacattgcgc aaaacaccgc atggaaaatc aacaagaaaatc tccctaggg cgccaaacgtt 10200
atcaccaagt ggaaggattt tccggctcgag gacatccctg cgattgagcg tgaagaactc 10800
ccgatgaaac cggaagacat cgacatgaat cctgaggcgt tcacccgcgt gaaacgtgt 11400
gcccgtgtt gttaccgcaaa ggacaaggctt cgcaagtttc gccgtatcag ctttgggttc 12000
atgcttgagc aagccaataa gtttgcataac cataaggcca tctgggtcccc ttacaacatg 12600
gactggcgcg tgcgtgtttt cgtgtgtca atgttcaacc cgcaaggtaa cgatgtacc 13200
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggtt aggaaggtaa ctactggctg 13800
aaaatccacg gtgcaaactg tgccgggtgtc gataagggtt cgttccctga ggcgtatcaag 14400
ttcattgagg aaaaccacgca gaacatcatg gcttgcgttca agtctccact ggagaacact 15000
tgggtggctgtt agcaagattt tccgttctgc ttcccttggtt tctgctttga gtacgctggg 15600
gtacagcacc acggcctgag ctataactgc tccctccgc tggcggttga cgggtcttc 16200
tctggcatcc agcacttctc cgcgtatgtc cgagatgagg taggtggctcg cgcgggttac 16800
ttgcttccta gtgaaaccgt tcaggacatc tacgggattt tgcataagaa agtcaacgag 17400
attctacaag cagacgcaat caatgggacc gataacgaa tagttaccgtt gaccgatgag 18000
aacactggtg aaatctctga gaaagtcaag ctgggcacta aggcaactggc tggtaatgg 18600
ctggcttacg gtgttactcg cagtgtgtactt aagcggttcag tcatgtacgtt ggcttacggg 19200
tccaaagagt tcgggttccg tcaacaagtg ctggaaagata ccattcagcc agctattgtt 19800
tccggcaagg gtctgtatgtt cactcagccg aatcaggctg ctggatacat ggctaaagctg 20400
atttggaaat ctgtgagcgtt gacgggtggta gctgcgggtt aagcaatgaa cgggttacaaag 21000
tctgctgtca agtgcgtggc tgctgaggcgtt aaagataaga agactggaga gattttcgc 21600
aaggcgttgcg ctgtgcattt ggtaacttcc gatggttcc tcatgtggca ggaatacaag 22200

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aagcctattc agacgcgtt gaacctgatg ttccctcggtc agttccgcctt acagcctacc	2280
atataaccca acaaagatag cgagattgtat gcacacaaac aggagtctgg tatacgctcct	2340
aactttgtac acagccaaga cggtagccac cttcgtaaaga ctgttagtgtg ggcacacgag	2400
aagtacggaa tcgaatcttt tgcaactgatt cacgactcct tcggtaccat tcggctgac	2460
gtctgcgaacc tggtaaaggc agtgcgcgaa actatggttt acacatatga gtcttgtat	2520
gtactggctg atttctacga ccagttcgtt gaccagtgc acgagtctca attggacaaa	2580
atgccagcac ttccggctaa aggtaacttg aacctccgtg acatctttaga gtccggacttc	2640
gcgttcgcgt aa	2652

<210> SEQ ID NO 32

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 32

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu			
1	5	10	15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu			
20	25	30	

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu			
35	40	45	

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val			
50	55	60	

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys			
65	70	75	80

Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg			
85	90	95	

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu			
100	105	110	

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser			
115	120	125	

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala			
130	135	140	

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys			
145	150	155	160

His Phe Lys Lys Asn Val Glu Gln Leu Asn Lys Arg Val Gly His			
165	170	175	

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser			
180	185	190	

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp			
195	200	205	

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr			
210	215	220	

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp			
225	230	235	240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr			
245	250	255	

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val			
260	265	270	

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala			
275	280	285	

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala

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290	295	300
Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile		
305	310	315
320		
Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala		
325	330	335
Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile		
340	345	350
Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp		
355	360	365
Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val		
370	375	380
Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe		
385	390	395
400		
Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe		
405	410	415
Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe		
420	425	430
Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys		
435	440	445
Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly		
450	455	460
Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys		
465	470	475
480		
Phe Ile Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro		
485	490	495
Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu		
500	505	510
Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr		
515	520	525
Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln		
530	535	540
His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn		
545	550	555
560		
Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys		
565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn		
580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys		
595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly		
610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly		
625	630	635
640		
Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln		
645	650	655
Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln		
660	665	670
Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr		
675	680	685
Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys		
690	695	700
Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg		
705	710	720

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Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> SEQ ID NO 33
<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 33

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ttcaaacatc tggctgacca ttacggtgag cgtttagctc gccaacagt ggcccttgag	120
catgagtctt acgagatggg tgaaggcacgc ttccgcaaga tgtttgagcg tcaacttaaa	180
gctgggtgagg ttgcggataa cgctgccgc aagcctctca tcactaccct actccctaag	240
atgattgcac acatcaacga ctggtttgag gaagtgaaag ctaagegcgg caagegcgg	300
acagccttcc agttcttgca agaaaatcaag cggaaagccg tagcgtacat caccattaag	360
accactctgg cttgccttaac cagtgctgac aatacaaccg ttcaggctgt agcaagcgca	420
atcggtcggg ccatttggaa cgaggctcgc ttccggctgta tccgtgacct tgaagctaa	480
cacttcaaga aaaacgttga ggaacaactc aacaagcgcg tagggcacgt ctacaagaaa	540
gcatttatgc aagtttgcgaa ggctgacatg ctctctaagg gtctactcgg tggcgaggcg	600
tggtcttcgt ggcataagga agactctatt catgttaggag tacgctgcat cgagatgtc	660
attgagtcaa ccggaatgggt tagtttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaaactcgc acctgaatac gctgaggctta tcgcaacccg tgcaggctgc	780
ctggctggca tctctccgat gttccaaacct tgcgttagttc ctccctaagcc gtggactggc	840
attactgggt gtggcttattg ggctaacggc cgtcgctcgc tggcgctgggt gcgtactcac	900
agtaagaaag cactgatgcg ctacgaagac gtttacatgc ctgagggtta caaagcgatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tccttagcggt cgccaacgta	1020
atcaccaagt ggaagcattt tccggctcgag gacatccctg cgattgagcg tgaagaactc	1080
ccgatgaaac cggaaagacat cgacatgaat cctgaggctc tcaccgcgtg gaaacgtgct	1140

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ggcgctgctg tgcgttgcggaa ggacaaggct cgcaagtctc ggcgtatcag ccttgaggttc 1200
atgcgttgcgc aagccataac gtttgcatac cataaggccc tctggttccc ttacaacatg 1260
gactggcgcg gtctgttttgcgtgtca atgttcaacc cgcaaggtaa cgatatgacc 1320
aaaggactgc ttacgtggc gaaaggtaaa ccaatcggtt aaggaaggtaa ctactggctg 1380
aaaatccacg gtgcacaaactg tgccgggtgtc gataaggttc cgttccctga ggcgcataag 1440
ttcatttgcgg aaaaccacga gaacatcatg gtttgcgtca agtcttcact ggagaacact 1500
ttggtggctg agcaagattc tccgttctgc ttcccttgcgt tctgcttga gtacgctgg 1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcggttga cgggtctgc 1620
tctggcatcc agcacttctc cgcgatgtc cgagatgagg taggtggtgc cgccgttaac 1680
ttgcttcata gtgaaaccgt tcaggacatc tacgggatttgc ttgctaagaa agtcaacgag 1740
attctacaag cagacgcaat caatgggacc gataacgaag tagttaccgt gaccgatgag 1800
aacactggtg aaatctctga gaaagtcaag ctggcacta aggcaactggc tggtaatgg 1860
ctggcttacg gtgttactcg cagtgtgact aagcggttgcgt tcatgacgct ggcttacggg 1920
tccaaagagt tcggcttccg tcaacaagtgc ctggaaaggta ccattcagcc agtctattgat 1980
tccggcaagg gtctgtatgtt cactcagccg aatcaggctg ctggatacat ggctaaagctg 2040
atttggaaat ctgtgagcgt gacgggtggta gctgcgggttgc aagcaatgaa ctggcttaag 2100
tctgctgcttgc agtctgtggc tgctgagggtc aaagataaga agactggaga gattttcgc 2160
aagcggttgcg ctgtgcatttggtaactctt gatggttcc ctgtgtggca ggaatacaag 2220
aagcctattc agacgcgcctt gaacctgtatc ttcctcggtc agttccgcctt acagcctacc 2280
attaacacca acaaagatag cgagattgtatc gcacacaaac aggagtctgg tatcgctcct 2340
aactttgtac acagccaaga cggtagccac cttcgtaaagaa ctgttagtgc ggcacacgag 2400
aagtacggaa tcgaatcttt tgcaactgatt cacgactcct tcggtaatcat tccggctgac 2460
gctgcgaacc tggtaaagc agtgcgcgaa actatggttgc acacatatga gtcttgcgt 2520
gtactggctg atttctacga ccagttcgctt gaccagttgc acgagtctca attggacaaa 2580
atgccagcac ttccggctaa aggttaacttg aacctccgtt acatctttaga gtcggacttc 2640
gegttgcgtt aa 2652

```

<210> SEQ ID NO 34

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 34

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1															
															15

Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu
															20
															25
															30

Ala	Arg	Glu	Gln	Leu	Ala	Ile	Glu	His	Glu	Ser	Tyr	Glu	Met	Gly	Glu
															35
															40
															45

Ala	Arg	Phe	Arg	Lys	Met	Phe	Glu	Arg	Gln	Leu	Lys	Ala	Gly	Glu	Val
															50
															55
															60

Ala	Asp	Asn	Ala	Ala	Ile	Lys	Pro	Leu	Ile	Thr	Thr	Leu	Leu	Pro	Lys
															65
															70
															75
															80

Met	Ile	Ala	His	Ile	Asn	Asp	Trp	Phe	Glu	Glu	Val	Lys	Ala	Lys	Arg
															85
															90
															95

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu

-continued

100	105	110
Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser		
115	120	125
Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala		
130	135	140
Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys		
145	150	155
His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His		
165	170	175
Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser		
180	185	190
Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp		
195	200	205
Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr		
210	215	220
Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp		
225	230	235
240		
Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr		
245	250	255
Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val		
260	265	270
Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala		
275	280	285
Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala		
290	295	300
Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile		
305	310	315
320		
Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala		
325	330	335
Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile		
340	345	350
Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp		
355	360	365
Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Val		
370	375	380
Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe		
385	390	395
400		
Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe		
405	410	415
Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe		
420	425	430
Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys		
435	440	445
Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly		
450	455	460
Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys		
465	470	475
480		
Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro		
485	490	495
Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu		
500	505	510
Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr		
515	520	525

-continued

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
 530 535 540
 His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
 545 550 555 560
 Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
 565 570 575
 Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
 580 585 590
 Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
 595 600 605
 Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
 610 615 620
 Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
 625 630 635 640
 Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln
 645 650 655
 Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Thr Gly Glu Ile Leu Arg
 705 710 715 720
 Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
 725 730 735
 Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
 740 745 750
 Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
 755 760 765
 Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
 770 775 780
 Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
 785 790 795 800
 Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
 805 810 815
 Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
 820 825 830
 Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
 835 840 845
 Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
 850 855 860
 Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
 865 870 875 880
 Ala Phe Ala

<210> SEQ ID NO 35
 <211> LENGTH: 2652
 <212> TYPE: DNA
 <213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 35

atgaacacgtaaacatcgcttacaacgcgttctctgacatcgactggctgcttatcccc 60

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catgagtctt acgagatggg tgaagcacgc ttccgcaaga tgtttgagcg tcaacttaaa	180
gttgtgagg ttgcggataa cgctgccgc aagcctctca tcactaccct actccctaag	240
atgattgcac acatcaacga ctggtttag gaagtgaaa ctaagegcgg caagegcgg	300
acagccttc agttctgca agaaatcaag ccggaagccg tagcgtacat caccattaag	360
accactctgg cttgectaac cagtgctac aatacaaccg ttcaaggctgt agcaagcgca	420
atcggtcggg ccattgagga cgaggctcg ttcggctgta tccgtgacct tgaagctaag	480
cacttcaaga aaaacgttga ggaacaactc aacaagcgc tagggcacgt ctacaagaaa	540
gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcg tggcgaggcg	600
tggcttcgt ggcataagga agactctatt catgttaggg tacgctgcat cgagatgct	660
attgagtcaa ccggaatggg tagtttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcgc acctgaatac gctgaggcta tcgcaacccg tgcaggctgc	780
ctggctggca tctctccgat gttccaaacct tgcgttagtt ctcctaagcc gtggacttggc	840
attactgggt gtggcttattt ggctaacggg cgtcgcttc tggcgcttggt gcgtactcac	900
agtaagaaag cactgatgac ctacgaagac gtttacatgc ctgagggtgta caaagcgatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaaatc tcctagcggt cgccaaacgta	1020
atcaccaagt ggaagcattt tccggctcgag gacatccctg cgattgagcg tgaagaactc	1080
ccgatgaaac cggaaagacat cgacatgaat cctgaggctc tcaccgcgtg gaaacgtgct	1140
gccgctgctg tgtaccgcaa ggacaaggct cgcaagtctc gccgtatcag ccttgagttc	1200
atgcttgcgc aagccaataa gtttgctaac cataaggccc tctggttccc ttacaacatg	1260
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatgtgacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggtt aggaaggtaa ctactggctg	1380
aaaaatccacg gtgcaaactg tgccgggtgc gataaggctc cgttccctga gcgcatcaag	1440
ttcattgagg aaaaccacga gaacatcatg gtttgcgtta agtctccact ggagaacact	1500
tggggctg agcaagattt tccgttctgc ttcccttgcgt tctgcttgg tgcgtctgg	1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcgttga cgggtctgc	1620
tctggcatcc agcacttctc cgcgatgtctc cgagatgagg taggtggctcg cgccgttaac	1680
ttgcttccca gtgaaaccgt tcaggacatc tacgggattt ttgcttaagaa agtcaacgag	1740
attctacaag cagacgcaat caatgggacc gataacgaa tagttaccgt gaccgtatgag	1800
aacactggtg aaatctctga gaaagtcaag ctggcacta aggactggc tggtaatgg	1860
ctggcttacg gtgttactcg cagtgtgact aagcgttcaag tcatgacgtt ggcttacggg	1920
tccaaagagt tcggcttccg tcaacaagtg ctggaaagata ccattcagcc agctattgtat	1980
tcggcaagg gtctgtatgtt cactcagccg aatcaggctc ctggatacat ggctaaatgt	2040
atttggaaat ctgtgagcgt gacggtggtt gctgcgggtt aagcaatgaa cgggtttaa	2100
tctgctgcta agctgctggc tgctgaggctc aaagataaga agactggaga gattttcg	2160
aagcgttgcg ctgtgcattt ggttactctt gatggttcc ctgtgtggca ggaatacaag	2220
aagccttattc agacgcgcgtt gaaacctgtatg ttccctcggtc agttccgcgtt acagcctacc	2280
attaacacca acaaagatag cgagatgtat gcaacacaac aggactctgg tatacgctct	2340
aactttgtac acagccaaga cggtagccac ctgcgtaaat ctgtgtgtt ggcacacgag	2400
aagtacggaa tcgaatcttt tgcactgatt cacgactcct tcggtaccat tcggctgac	2460

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gctgcgaacc tggtaaaaggc agtgcgcgaa actatggttg acacatatga gtcttgat 2520
gtactggctg atttctacga ccagttcgct gaccagttgc acgagtctca attggacaaa 2580
atgccagcac ttccggctaa aggtaacttg aacctccgtg acatcttaga gtcggacttc 2640
gcgttcgcgt aa 2652

```

```

<210> SEQ_ID NO 36
<211> LENGTH: 883
<212> TYPE: PRT
<213> ORGANISM: T7 bacteriophage

```

```
<400> SEQUENCE: 36
```

```

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
1 5 10 15

```

```

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
20 25 30

```

```

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
35 40 45

```

```

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
50 55 60

```

```

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
65 70 75 80

```

```

Met Ile Ala His Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
85 90 95

```

```

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
100 105 110

```

```

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
115 120 125

```

```

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
130 135 140

```

```

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
145 150 155 160

```

```

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
165 170 175

```

```

Val Tyr Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
180 185 190

```

```

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
195 200 205

```

```

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
210 215 220

```

```

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
225 230 235 240

```

```

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
245 250 255

```

```

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
260 265 270

```

```

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
275 280 285

```

```

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
290 295 300

```

```

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
305 310 315 320

```

```

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
325 330 335

```

-continued

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe
405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

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Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> SEQ_ID NO 37

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 37

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ttcaacactc tggctgacca ttacggtag cgtttagctc gcgaacagtt ggccctttag	120
catgagtctt acgagatggg tgaagcacgc ttccgcaaga tggtagcg tcaacttaaa	180
gttgttggagg ttgcggataa cgctgccgc aagcctctca tcactaccct actccctaag	240
atgattgcac acatcaacga ctggtttag gaaatgaaag ctaagcgccg caagcgccg	300
acagccttcc agttctgca agaaatcaag ccggaaagccg tagcgtacat caccattaag	360
accactctgg cttgcctaac cagtgcgtac aatacaaccg ttcaggctgt agcaagcgca	420
atcggtcggtt ccatttgagga cgaggctcgc ttccgtcgta tccgtgacat tgaagctaa	480
cacttcaaga aaaacgttga ggaacaactc aacaagcgcc tagggcacgt ctacaagaaa	540
gcatttatgc aagtgtcga ggctgacatg ctctctaagg gtctactcgg tggcgaggcg	600
tggcttcgt ggcataagga agactctatt catgttaggag tacgctgcat cgagatgtc	660
attgagtcaa ccgaaatggg tagtttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcgc acctgaatac gctgaggctc tcgcacccg tgcaggtgc	780
ctggctggca tctctccat gttcaaccc tgcgttagttc ctccataagcc gtggacttgc	840
attactggtg gtggctattt ggcttaacggt cgtcgctc tggcgctggt gcgtactcac	900
agtaagaaag cactgtgcg ctacaaagac gtttacatgc ctgagggtta caaagcgatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tcctagcggt cgccaacgta	1020
atcacaagg ggaaggattt tccggctcgag gacatccctc cgattgagcg tgaagaactc	1080
ccgatgaaac cggaaagacat cgacatgaat cctgaggctc tcaccgcgtg gaaacgtgct	1140
gccgctgctg tgtaccgcaa ggacaaggct cgcaagtctc gccgtatcag ccttgagttc	1200
atgcttgcgc aagccaataa gtttgcatac cataaggccc tctggttccc ttacaacatg	1260
gactggcgcc gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggttta aggaaggtaa ctactggctg	1380

-continued

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aaaatccacg gtgcaaactg tgccgggtgc gataaggttc cgccccctga gcgcataag 1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgcta agtctccact ggagaacact 1500
tggtgtggctg agcaagattc tccgttctgc ttcccttgcgt tctgctttga gtacgctgg 1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcggttga cgggtcttc 1620
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aacactggtg aaatctctga gaaagtcaag ctgggcacta aggcaactggc tggtcaatgg 1860
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tccaaagagt tcggcttcgg tcaacaagtgc ctggaaagata ccattcagcc agcttattgat 1980
tccggcaagg gtctgtatgtt cactcagccg aatcaggctg ctggatacat ggctaaagctg 2040
atttggaaat ctgtgagcgt gacgggttgc gctgcgggtt aagcaatgaa ctggcttaag 2100
tctgctgcta agctgctggc tgctgaggc aaagataaga agactggaga gattcttcgc 2160
aagcggttgcg ctgtgcattt ggttaactctt gatggttcc ctatgtggca ggaataacaag 2220
aagccttattt agacgcgcgtt gaacctgtat ttccctcggtc agttccgc acagcttacc 2280
attaacacca acaaagatag cgagattgtt gcacacaaac aggagtctgg tatcgcttcc 2340
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aagtaacggaa tcgaatcttt tgcaactgatt cacgactctt tccggctgac 2460
gctgcgaacc ttttcaaaagc agtgcgcgaa actatggttt acacatatga gtcttgcgt 2520
gtactggctt atttctacga ccagttcgctt gaccaggctt acgagtctca attggacaaa 2580
atgccagcac ttccggctaa aggttaacttgc aaccccttgc acatcttgc gtcggacttc 2640
gcgttgcgtt aa 2652

```

<210> SEQ ID NO 38

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 38

```

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
1           5          10          15

```

```

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
20          25          30

```

```

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
35          40          45

```

```

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
50          55          60

```

```

Ala Asp Asn Ala Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
65          70          75          80

```

```

Met Ile Ala His Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
85          90          95

```

```

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
100         105         110

```

```

Ala Val Ala Tyr Ile Thr Ile Lys Thr Leu Ala Cys Leu Thr Ser
115         120         125

```

```

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
130         135         140

```

-continued

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 145 150 155 160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
 165 170 175

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
 245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
 260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
 275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
 290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
 305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
 370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe
 405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Trp Leu Lys Ile His Gly
 450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
 465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
 485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
 500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
 515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
 530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
 545 550 555 560

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Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> SEQ ID NO 39

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 39

atgaacacgca ttaacatcgca taagaacgac ttctctgaca tcgaactggc tgctatcccg 60

ttcaaacactc tggctgacca ttacggtag cgttagctc gccaacagtt ggcccttgag 120

catgagtctt acgagatggg tgaaggcacgc ttccgcaaga tgtttgagcg tcaacttaaa 180

gctggtgagg ttgcggataa cgctgccccc aagcctctca tcactaccct actccctaag 240

atgattgcac acatcaacga ctggtttag gaagtgaaag ctaagcgccgg caagcgcccg 300

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acagccttcc agttctcgca agaaaatcaag ccggaaagccg tagcgatcat caccattaag 360
accactctgg ctgcctaact cagtgtcgac aataacaaccg ttccaggctgt agcaagcgca 420
atcggtcggg ccattgagga cgaggctcg ttcgggtcgta tccgtgaccc tgaagctaaag 480
cacttcaaga aaaacgttga ggaacaactc aacaagcgcg tagggcacgt ctacaagaaa 540
gcatttatgc aagttgtcgaa ggctgacatg ctctctaagg gtctactcg tggcgaggcg 600
tgttcttcgt ggcataagga agactctatt catgttaggag tacgctgcat cgggatgctc 660
atttgagtcaa ccggaaatgtt tagtttacac cgccaaatgt ctggcgtagt aggtcaagac 720
tctgagacta tcgaactcg acctgaatac gctgaggcta tcgcaacccg tgcaggtcg 780
ctggctggca tctctccgtat gttccaaacct tgegttagtcc tcctctaaagcc gtggactggc 840
attactggtg gtggctatgt ggctaaccgt cgctcgatcc tggcgctgg tgcgtactcac 900
agtaagaaag cactgtatgc ctacgaaagac gtttacatgc ctgagggtta caaaacgatt 960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tcctagcggt cgccaaacgta 1020
atcaccaagt ggaagcatgt tccggctcgag gacatccctg cgattgagcg tgaagaactc 1080
ccgatgaaac cggaagacat cgacatgaaat cctgaggctc tcacccgcgt gaaacgtgt 1140
gcccgtctgt tgtaaccgcaaa ggacaaggct cgcaagtttc gccgtatcag ctttgcgtt 1200
atgcttgcgc aagccaataaa gtttgcatac cataaggeca tctgggtcccc ttacaacatg 1260
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc 1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggtt aggaagggtt ctactggctg 1380
aaaatccacg gtgcaaaactg tgccgggtgtc gataagggtt cttccctgt ggcgcataag 1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgttca agtctccact ggagaacact 1500
tggtggctg agcaagatc tccgttctgc ttcttgcgt tctgcttga gtacgctggg 1560
gtacagcacc acggccctgag ctataactgc tccttccgc tggcggttga cgggttgc 1620
tctggcatcc agcacttctc cgcgatgctc cgagatgagg taggtggctcg cgccgttaac 1680
ttgcttcataa gtgaaaccgt tcaggacatc tacgggattt tgctaaagaa agtcaacgag 1740
attctacaag cagacgcaat caatgggacc gataacgaaag tagttaccgt gaccgatgag 1800
aacactgggt aaatctctga gaaagtcaag ctgggcacta aggcaactggc tggtaatgg 1860
ctggcttacg gtgttactcg cagtgtgact aagcggttgc tcatgacgct ggcttacggg 1920
tccaaagagt tcggctccg tcaacaagtg ctggaaagata ccattcagcc agctattgt 1980
tccggcaagg gtctgatgtt cactcagccg aatcaggctg ctggatacat ggctaaagctg 2040
atttggaaat ctgtgagcgt gacgggttgc gctgcgggtt aagcaatgaa cgggttcaag 2100
tctgctgcttca agctgtgttgc tgctgaggctc aaagataaga agactggaga gattttcg 2160
aagcggttgc ctgtgcattt ggttaactctt gatggttccct ctgtgtggca ggaatacaag 2220
aagccttatttcc agacgctgtt gaaacctgtatg ttccctcggtc agttccgtt acagcctacc 2280
attaacacca acaaagatag cgagattgtt gcacacaaaac aggagttctgg tatcgcttct 2340
aactttgtac acagccaaaga cggtagccac ctgcgttgcgaa ctgttagtgc ggcacacgag 2400
aagtacggaa tcgaatcttt tgcaactgtt caccgactctt tccgggttgc gctgcgttgc 2460
gctgcgttgc accgttcaaaacg agtgcgttgcgaa actatgggtt gacatcatgaa gtcttgcgt 2520
gtactggctg atttctacga ccagttcgctt gaccagttgc acgagttctca attggacaaa 2580
atgccagcac ttccggctaa aggttaacttgc aacctccgtt acatcttgc gtcggacttc 2640

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gcgttcgcgt aa

2652

<210> SEQ ID NO 40
<211> LENGTH: 883
<212> TYPE: PRT
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 40

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1			5			10				15					
Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu
	20				25					30					
Ala	Arg	Glu	Gln	Leu	Ala	Leu	Glu	His	Glu	Ser	Tyr	Glu	Met	Gly	Glu
	35				40					45					
Ala	Arg	Phe	Arg	Lys	Met	Phe	Glu	Arg	Gln	Leu	Lys	Ala	Gly	Glu	Val
	50				55					60					
Ala	Asp	Asn	Ala	Ala	Ile	Lys	Pro	Leu	Ile	Thr	Thr	Leu	Leu	Pro	Lys
	65				70				75					80	
Met	Ile	Ala	His	Ile	Asn	Asp	Trp	Phe	Glu	Glu	Val	Lys	Ala	Lys	Arg
	85					90					95				
Gly	Lys	Arg	Pro	Thr	Ala	Phe	Gln	Phe	Leu	Gln	Glu	Ile	Lys	Pro	Glu
	100					105					110				
Ala	Val	Ala	Tyr	Ile	Thr	Ile	Lys	Thr	Thr	Leu	Ala	Cys	Leu	Thr	Ser
	115					120					125				
Ala	Asp	Asn	Thr	Thr	Val	Gln	Ala	Val	Ala	Ser	Ala	Ile	Gly	Arg	Ala
	130					135				140					
Ile	Glu	Asp	Glu	Ala	Arg	Phe	Gly	Arg	Ile	Arg	Asp	Leu	Glu	Ala	Lys
	145					150			155			160			
His	Phe	Lys	Asn	Val	Glu	Glu	Gln	Leu	Asn	Lys	Arg	Val	Gly	His	
	165					170			175			175			
Val	Tyr	Lys	Ala	Phe	Met	Gln	Val	Val	Glu	Ala	Asp	Met	Leu	Ser	
	180					185			190			190			
Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp	Ser	Ser	Trp	His	Lys	Glu	Asp
	195					200			205			205			
Ser	Ile	His	Val	Gly	Val	Arg	Cys	Ile	Glu	Met	Leu	Ile	Glu	Ser	Thr
	210					215			220			220			
Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn	Ala	Gly	Val	Val	Gly	Gln	Asp
	225					230			235			240			
Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro	Glu	Tyr	Ala	Glu	Ala	Ile	Ala	Thr
	245					250			255			255			
Arg	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser	Pro	Met	Phe	Gln	Pro	Cys	Val
	260					265			270			270			
Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile	Thr	Gly	Gly	Tyr	Trp	Ala	
	275					280			285			285			
Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val	Arg	Thr	His	Ser	Lys	Lys	Ala
	290					295			300			300			
Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met	Pro	Glu	Val	Tyr	Lys	Ala	Ile
	305					310			315			320			
Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys	Ile	Asn	Lys	Lys	Val	Leu	Ala
	325					330			335			335			
Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys	His	Cys	Pro	Val	Glu	Asp	Ile
	340					345			350			350			
Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro	Met	Lys	Pro	Glu	Asp	Ile	Asp
	355					360			365			365			

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Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
 370 375 380
 Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400
 Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe
 405 410 415
 Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430
 Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445
 Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
 450 455 460
 Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
 465 470 475 480
 Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
 485 490 495
 Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
 500 505 510
 Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
 515 520 525
 Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
 530 535 540
 His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Arg Ala Val Asn
 545 550 555 560
 Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
 565 570 575
 Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
 580 585 590
 Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
 595 600 605
 Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
 610 615 620
 Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
 625 630 635 640
 Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln
 645 650 655
 Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
 705 710 715 720
 Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
 725 730 735
 Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
 740 745 750
 Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
 755 760 765
 Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
 770 775 780
 Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu

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785	790	795	800
Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr			
805		810	815
Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met			
820		825	830
Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln			
835		840	845
Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu			
850		855	860
Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe			
865		870	875
Ala Phe Ala			

<210> SEQ ID NO 41

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 41

atgaacacgtaa	ttacatcgca	taagaacgac	ttctctgaca	tgcgactggc	tgctatcccg	60
ttcaacactc	tggctgacca	ttacggtag	cgtttagtc	gogaacagtt	ggcccttgag	120
catgagtctt	acgagatggg	tgaaggcacgc	ttccgcaaga	tgttgtgagcg	tcaacttaaa	180
gctggtgagg	ttgcggataa	cgctgccgccc	aaggctctca	tcactaccct	actccctaag	240
atgattgcac	acatcaacgta	ctgggtttag	gaagtgaaaag	ctaagegcgg	caagegcgg	300
acagccttcc	agttcctgca	agaaatcaag	ccggaaagccg	tagcgtacat	caccattaag	360
accactctgg	cttgccataac	cagtgtac	aatacaaccg	tgcaggctgt	agcaagcgca	420
atcggtcggg	ccattgagga	cgaggctcg	ttcggtegta	tccgtgacct	tgaagctaa	480
cacttcaaga	aaaacgttga	ggaacaactc	aacaagcgcg	tagggcacgt	ctacaagaaa	540
gcatttatgc	aagtgtcgaa	ggctgacatg	ctctctaagg	gtctactcg	tggcgaggcg	600
tggcttcgt	ggcataagga	agactctatt	catgttaggg	tacgctgcat	cgagatgtc	660
attgagtcaa	ccggaatgg	tagtttacac	cgccaaaatg	ctggcgtagt	aggtcaagac	720
tctgagacta	tcgaactcg	acctgaatac	gtggggctca	tgcgcaaccgg	tgcagggtcg	780
ctggctggca	tctctccgat	gttccaacct	tgcgttagttc	ctccataagcc	gtggactggc	840
attactggtg	gtggctattg	ggctaacgg	cgtcgctc	tggcgctgtt	gcgtactcac	900
agtaagaaag	cactgtatgc	ctacgaagac	gtttacatgc	ctgagggtgt	caaagcgatt	960
aacattgcgc	aaaacaccgc	atggaaaatc	aacaagaaag	tccttagcggt	cgccaaacgta	1020
atcaccaagt	ggaaggattt	tccggtcgag	gacatccctg	cgattgagcg	tgaagaactc	1080
ccgatgaaac	cggaagacat	cgacatgaat	cctgaggctc	tcacccgcgt	gaaacgtgt	1140
gccgctgctg	tgtacccgaa	ggacaaggct	cgcaagtctc	gccgtatcag	ccttgagttc	1200
atgcttgagc	aagccaataa	gtttgctaac	cataaggcca	tctggttccc	ttacaacatg	1260
gactggcg	gtcgttta	cgtgtgtca	atgttcaacc	cgcaaggtaa	cgatgtgacc	1320
aaaggactgc	ttacgctggc	gaaaggtaaa	ccaatcgta	aggaaggta	ctactggct	1380
aaaatccacg	gtgcaaaactg	tgcgggtgtc	gataaggttc	cgttccctga	gccccatcaag	1440
ttcattgagg	aaaaccacga	gaacatcatg	gcttgcgtca	agtctccact	ggagaacact	1500
tggtggctg	agcaagattc	tccgttctgc	ttccttgct	tctgctttga	gtacgctggg	1560

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gtacagcacc acggcctgag ctataactgc tcccttcgc tggcggttga cgggtctgc	1620
tctggcatcc agcaattctc cgcgatgctc cgagatgagg taggtggtcg cgccgtaac	1680
ttgcttcta gtgaaaccgt tcaggacatc tacgggattt ttgctaagaa agtcaacgag	1740
attctacaag cagacgcaat caatggacc gataacgaag tagttaccgt gaccgatgag	1800
aacactggtg aaatctctga gaaagtcaag ctgggcacta aggcaactggc tggtaatgg	1860
ctggcttacg gtgttactcg cagtgtgact aagcgttacg tcatgacgct ggcttacggg	1920
tccaaagagt tcggcttccg tcaacaagtg ctggaaaggta ccattcagcc agctattgat	1980
tccggcaagg gtctgatgtt cactcagccg aatcaggctg ctggatacat ggctaagctg	2040
atttggaaat ctgtgagcgt gacgggtgta gctgcgggaa aagcaatgaa ctggcttaag	2100
tctgctgctca agctgctggc tgctgaggctc aaagataaga agactggaga gattttcgc	2160
aagcggtgcg ctgtgcattt ggttaactctt gatggttcc ctagtggca ggaatacaag	2220
aagcctatttca agacgcgcctt gaacctgtatg ttccctcggtc agttccgcctt acagcctacc	2280
attaacaccca acaaagatag cgagattgtat gcacacaaaac aggagtctgg tatcgctcct	2340
aactttgtac acagccaaga cggttagccac cttcgtaaga ctgttagtgg ggcacacgag	2400
aagtacggaa tcgaatcttt tgcaactgatt cacgactcct tcggtaaccat tccggctgac	2460
gctgcgaacc tggtcaaaagc agtgcgcgaa actatggttt acacatatga gtcttgtat	2520
gtactggctg atttctacga ccagttcgct gaccagttgc acgagtctca attggacaaa	2580
atgccagcac ttccggctaa aggttaacttg aacctccgtg acatctttaga gtcggacttc	2640
gcgttcgcgt aa	2652

<210> SEQ_ID NO 42

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 42

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu			
1	5	10	15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu			
20	25	30	

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu			
35	40	45	

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val			
50	55	60	

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys			
65	70	75	80

Met Ile Ala His Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg			
85	90	95	

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu			
100	105	110	

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser			
115	120	125	

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala			
130	135	140	

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys			
145	150	155	160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His			
165	170	175	

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Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe
405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys

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595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly		
610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly		
625	630	635
Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln		
645	650	655
Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln		
660	665	670
Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr		
675	680	685
Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys		
690	695	700
Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg		
705	710	715
Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp		
725	730	735
Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu		
740	745	750
Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu		
755	760	765
Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His		
770	775	780
Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu		
785	790	795
Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr		
805	810	815
Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met		
820	825	830
Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln		
835	840	845
Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu		
850	855	860
Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe		
865	870	875
Ala Phe Ala		

<210> SEQ_ID NO 43
<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 43

atgaacacga ttaacatcgc taagaacgac ttctctgaca tcgaactggc tgctatcccg	60
ttcaacactc tggctgacca ttacggtag cgtttagctc gcgaaacagtt ggcccttgag	120
catgagtctt acgagatggg tgaaggcacgc ttccgcaaga tggttgagcg tcaacttaaa	180
gtgtggtagg ttgcggataa cgctgccccc aagcctctca tcaactaccct actccctaag	240
atgattgcac acatcaacga ctgggtttag gaagtgaag ctaaggccgg caagcgcccc	300
acaggcttcc agttcctgca agaaaatcaag ccggaaagccg tagcgtacat caccattaag	360
accactctgg cttgcctaac cagtgctgac aataacaaccg ttcaaggctgt agcaagcgca	420
atcggtcgaa ccattgagga cgaggctcgc ttccgtcgta tccgtgaccc tgaagctaa	480

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cacttcaaga aaaacgttga ggaacaactc aacaagcgct tagggcacgt ctacaagaaa 540
gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcgg tggcgaggcg 600
tggcttcgtt ggcataagga agactctatt catgttaggag tacgctgcat cgagatgctc 660
attgagtcaa ccggaatgg tagcttacac cgccaaatg ctggcgtagt aggtcaagac 720
tctgagacta tcgaactcgc acctgaatac gctgaggceta tcgcaacccg tgcaggcgtc 780
ctggctggca tctctccgtat gttccaacct tgcttagttc ctccctaaagcc gtggactggc 840
attactgggt gtggctatgt ggctaacggg cgtcgctcc tggcgctgg gcgtactcac 900
agtaagaaag cactgatgcg ctacgaagac gtttacatgc ctgagggtgtaa caaagcgatt 960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tcttagcggt cgccaaacgta 1020
atcaccaagt ggaagcatgt tccggctcgag gacatccctg cgattgagcg tgaagaactc 1080
ccgtatgaaac cggaagacat cgacatgaat cctgaggceta tcaccgcgtg gaaacgtgt 1140
gccgctgtgtg tgcgttgcgaa ggacaaggct cgcaagtctc gccgtatcag cctttagttc 1200
atgcttgagc aagccaataa gtttgcatac cataaggcca tctggttccc ttacaacatg 1260
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatgtgacc 1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggtt aggaaggtaa ctactggctg 1380
aaaatccacg gtgcaaaactg tgcgggtgtc gataaggttc cttccctga ggcgtatcaag 1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgta agtctccact ggagaacact 1500
tggtgggtgtc agcaagatgtc tccgttctgc ttcccttgcgt tctgtttga gtacgctggg 1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcggttga cgggttgc 1620
tctggcatcc agcaacttctc cgcgtatgcg ctagatgggg taggtgtgtc cgcggtaac 1680
ttgcttcota gtgaaaccgt tcaggacate tacgggattt ttgctaaagaa agtcaacgag 1740
attctacaag cagacgcaat caatgggacc gataacgaa tagttaccgt gaccgatgag 1800
aacactgggt aaatctctga gaaagtcaag ctggggacta aggcaactggc tggtaatgg 1860
ctggcttacg gtgttactcg cagtgtgact aagcgttcaag tcatgacgct ggcttacggg 1920
tccaaagagt tggcttcgg tcaacaagtg ctggaaagata ccattcagcc agctattgt 1980
tccggcaagg gtctgtgtt cactcagccg aatcaggctg ctggatacat ggctaaagctg 2040
atttggaaat ctgtgacggt gacgggtgtt gctgcgggtt aagcaatgaa cgggttaag 2100
tctgctgtca agctgtggc tgctgagggtc aaagataaga agactggaga gattttcgc 2160
aagcgttgcg ctgtgcattt ggttaacttcc gatggttcc ctatgtggca ggaatacaag 2220
aagccttattc agacgacgtt gaaacctgtt ttctcggtc agttccgtt acagcctacc 2280
attaacacca acaaagatag cgagattgtt gcacacaac aggagctgg tatcgctcct 2340
aactttgtac acagcacaaga cggtagccac ctctgttgcgaa ctgttagtgc ggcacacgag 2400
aagtacggaa tcgaatcttt tgcaactgatt cacgactctt tgggttccat tccggctgac 2460
gctgcgaacc tggtaaaacgtt ggtgcgcgaa actatgggtt acacatgttgc tcttgcgt 2520
gtactggctgtt atttctacga ccagttcgtt gaccagggttgc acgagatctca attggacaaa 2580
atgccagcac ttccggctaa aggttaacttgc aacccctccgtt acatcttgc gtcggacttc 2640
qcgttcqcgaa 2652

<210> SEQ ID NO 44

<211> LENGTH: 883

<212> TYPE: PRT

<212> TYPE: PRI
<213> ORGANISM: T7 bacteriophage

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<400> SEQUENCE: 44

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
 1 5 10 15
 Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
 20 25 30
 Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
 35 40 45
 Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
 50 55 60
 Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
 65 70 75 80
 Met Ile Ala His Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
 85 90 95
 Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
 100 105 110
 Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
 115 120 125
 Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
 130 135 140
 Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 145 150 155 160
 His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
 165 170 175
 Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 180 185 190
 Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 195 200 205
 Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 210 215 220
 Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 225 230 235 240
 Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
 245 250 255
 Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
 260 265 270
 Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
 275 280 285
 Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
 290 295 300
 Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
 305 310 315 320
 Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 325 330 335
 Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 340 345 350
 Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 355 360 365
 Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Val
 370 375 380
 Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400
 Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe

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405	410	415
Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe		
420	425	430
Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys		
435	440	445
Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly		
450	455	460
Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys		
465	470	475
Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro		
485	490	495
Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu		
500	505	510
Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr		
515	520	525
Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln		
530	535	540
His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn		
545	550	555
Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys		
565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn		
580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys		
595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly		
610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly		
625	630	635
Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln		
645	650	655
Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln		
660	665	670
Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr		
675	680	685
Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys		
690	695	700
Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg		
705	710	715
Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp		
725	730	735
Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu		
740	745	750
Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu		
755	760	765
Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His		
770	775	780
Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu		
785	790	795
Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr		
805	810	815
Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met		
820	825	830

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Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> SEQ ID NO 45

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 45

atgaacacga ttaacatcg	taagaacgac ttctctgaca tcgaactggc tgctatccg	60
ttcaacactc tggctgacca ttacggtgag cgtttagctc gccaacagt	tttgcgtttag	120
catgagtctt acggatgtgg tgaaggcacgc ttccgcaaga tgtttgagcg	tcaacttaaa	180
gtcggtgagg ttgcggataa cgctgccccc aagcctctca tcaactaccct	actccctaag	240
atgattgcac gcatcaacga ctggttttag gaagtgaaag ctaagcgccg	caagcgcccc	300
acagccttcc agttcctgca agaaaatcaag ccggaaggccg tagcgtacat	caccattaag	360
accactctgg cttgccttaac cagtgcgtac aataacaaccg ttcaaggctgt	agcaagcgca	420
atcggtcggg ccattttagga cgaggctcgc ttccgtcgta tccgtgacct	tgaagctaag	480
cacttcaaga aaaacgttga ggaacaactc aacaaggcg tagggcacgt	ctacaagaaa	540
gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcgg	tggcgaggcg	600
tggcttcgtt ggcataagga agactctatt catgttaggag tacgctgtcat	cgagatgtc	660
attgagtcaa ccggaatgggt tagtttacac cgccaaaatg ctggcgtagt	aggtcaagac	720
tctgagacta tcgaactcgc acctgaatac gctgaggcta tcgcaaccgg	tgcaggtgcg	780
ctggctggca tctctccgat gttccaaacct tgcgttagttc ctccctaagcc	gtggactggc	840
attactgggtt gtggcttattt ggctaacccgt cgtcgctctc tggcgcttgtt	gcgtactcac	900
agtaagaaaag cactgtatgcg ctacgaagac gtttacatgc ctgagggtgt	caaaggcatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaaatg tccttagcggt	cgccaaacgta	1020
atcaccaagt ggaaggatttgc tccggcgtcag gacatccctg cgattgagcg	tgaagaactc	1080
ccgatgaaac cggaaagacat cgacatgaat cctgaggctc tcaccgcgtg	gaaacgtgct	1140
gecgctgctg tgcgttccaa ggacaaggct cgcgtatcgc ctttgatgtt	1200	
atgcgttgcg aagccaaataa gtttgcgtac cataaggccg tctgggtccc	ttacaacatg	1260
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa	cgatatgacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggttta aggaagggtt	ctactggctg	1380
aaaatccacg gtgcaactg tgccgggtgc gataaggttc cgttccctga	gcccacag	1440
ttcatttggggaaaaccacga gaacatcatg gcttgcgtca agtctccact	ggagaacact	1500
tggtggctgtg agcaagatttgc tccgttctgc ttcccttgcgt tctgcttgc	gtacgctggg	1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcggttgc	cggtcttgc	1620
tctggcatcc agcacttctc cgccgtgtctc cgagatgggg taggtggctcg	cgccgttaac	1680
ttgcttccta gtgaaaccgt tcaggacatc tacgggatttgc ttgctaaagaa	agtcaacgag	1740
attctacaag cagacgcaat caatggacc gataacgaa tagttaccgt	gaccgatgag	1800

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aacactggtg aaatctctga gaaagtcaag ctgggcacta aggcaactggc tggtaatgg 1860
ctggcttacg gtgttactcg cagtgact aagcgttacg tcatgacgtt ggcttacggg 1920
tccaaagagt tcggcttccg tcaacaagtg ctggaaaggta ccattcagcc agctattgat 1980
tccggcaagg gtctgatgtt cactcagccg aatcaggctg ctggatacat ggctaagctg 2040
atttggaaat ctgtgagcgt gacggtggtt gctgcggttt aagcaatgaa cgggcttaag 2100
tctgctgcta agctgctggc tgctgaggtc aaagataaga agactggaga gattttcgc 2160
aagcgttgcg ctgtgcattt ggttaactctt gatggttcc ctgtgtggca ggaataacaag 2220
aagcctattc agacgcgcctt gaacctgtat ttccctcggtt agttccgcctt acagectacc 2280
attaacacca acaaagatag cgagattgtat gcacacaaac aggagtctgg tatacgctct 2340
aactttgtac acagccaaga cggtagccac cttcgtaaga ctgttagtggc ggcacacgag 2400
aagtacggaa tcgaatcttt tgcaactgatt cacgactctt tccggctgac 2460
gtgtgcgaacc ttttcaaaac agtgcgcgaa actatggttt acacatatga gtcttggat 2520
gtactggctg atttctacga ccagttcgat gaccagttgc acgagtctca attggacaaa 2580
atgccagcac ttccggctaa aggtaacttg aacccctcgat acatctttaga gtcggacttc 2640
gggttcgcgt aa 2652

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<210> SEQ ID NO 46

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 46

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1															
															15

Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu
															30
20															

Ala	Arg	Glu	Gln	Leu	Ala	Leu	Glu	His	Glu	Ser	Tyr	Glu	Met	Gly	Glu
															45
35															

Ala	Arg	Phe	Arg	Lys	Met	Phe	Glu	Arg	Gln	Leu	Lys	Ala	Gly	Glu	Val
															60
50															

Ala	Asp	Asn	Ala	Ala	Ile	Lys	Pro	Leu	Ile	Thr	Thr	Leu	Leu	Pro	Lys
															80
65															

Met	Ile	Ala	Arg	Ile	Asn	Asp	Trp	Phe	Glu	Glu	Val	Lys	Ala	Lys	Arg
															95
85															

Gly	Lys	Arg	Pro	Thr	Ala	Phe	Gln	Phe	Leu	Gln	Glu	Ile	Lys	Pro	Glu
															110
100															

Ala	Val	Ala	Tyr	Ile	Thr	Ile	Lys	Thr	Leu	Ala	Cys	Leu	Thr	Ser	
															125
115															

Ala	Asp	Asn	Thr	Thr	Val	Gln	Ala	Val	Ala	Ser	Ala	Ile	Gly	Arg	Ala
															140
130															

Ile	Glu	Asp	Glu	Ala	Arg	Phe	Gly	Arg	Ile	Arg	Asp	Leu	Glu	Ala	Lys
															160
145															

His	Phe	Lys	Lys	Asn	Val	Glu	Glu	Gln	Leu	Asn	Lys	Arg	Val	Gly	His
															175
165															

Val	Tyr	Lys	Lys	Ala	Phe	Met	Gln	Val	Val	Glu	Ala	Asp	Met	Leu	Ser
															190
180															

Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp	Ser	Ser	Trp	His	Lys	Glu	Asp
															205
195															

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr

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210	215	220
Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp		
225	230	235 240
Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr		
245	250	255
Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val		
260	265	270
Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala		
275	280	285
Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala		
290	295	300
Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile		
305	310	315 320
Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala		
325	330	335
Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile		
340	345	350
Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp		
355	360	365
Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Val		
370	375	380
Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Ile Ser Leu Glu Phe		
385	390	395 400
Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe		
405	410	415
Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe		
420	425	430
Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys		
435	440	445
Gly Lys Pro Ile Gly Lys Glu Gly Tyr Trp Leu Lys Ile His Gly		
450	455	460
Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys		
465	470	475 480
Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro		
485	490	495
Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu		
500	505	510
Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr		
515	520	525
Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln		
530	535	540
His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Arg Ala Val Asn		
545	550	555 560
Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys		
565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn		
580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys		
595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly		
610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly		
625	630	635 640

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Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> SEQ ID NO 47

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 47

atgaacacgca ttaacatcgc taagaacgac ttctctgaca tcgaactggc tgctatcccg	60
ttcaacactc tggctgacca ttacggtag cgtttagtc gccaacagtt ggcccttgag	120
catgagtctt acgagatggg tgaaggcacgc ttccgcaaga tgtttgagcg tcaacttaaa	180
gtggtgagg ttgcggataa cgctgccgaa aagcctctca tcactaccct actccctaag	240
atgattgcac gcatcaacga ctgggtttag gaagtgaaa ctaagcgccg caagcgccc	300
acagccttcc agttcctgca agaaatcaag ccggaagccg tagcgtacat caccattaag	360
accactctgg cttgcctaac cagtgctgac aatacaaccg ttcaaggctgt agcaagcgca	420
atcgggtcgaa ccattgagga cgaggctcgc ttccgtcgta tccgtgacct tgaagctaa	480
cacttcaaga aaaacgttga ggaacaactc aacaagcgccg tagggcacgt ctacaagaaa	540
gcatttatgc aagttgcga ggctgacatg ctctctaagg gtctactcgg tggcgaggcg	600
tggcttcgt ggcataagga agactctatt catgtaggag tacgctgcat cgagatgctc	660
attgagtcaa ccggaatggg tagcttacac cgccaaaatg ctggcgtagt aggtcaagac	720

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tctgagacta tcgaaactcgc acctgaatac gctgaggcta tegcaaccgc tgccaggcg 780
ctggctggca tctctccgat gttccaacct tgegttagtc ctcttaagcc gtggactggc 840
attactgggt gtggctatg ggctaaccgt cgctgcttc tggcgctggt gctgactcac 900
agaagaag cactgatgcg ctacgaagac gttacatgc ctgagggtgt aaaaaggcatt 960
aacattgcgc aaaacaccgc atggaaaatc aacaagaag tcctagcggt cgccaaacgta 1020
atcaccaagt ggaagcatgt tccggctcgag gacatccctg cgattgagcg tgaagaactc 1080
ccgatgaaac cggaagacat cgacatgaat cctgaggctc tcaccgcgtg gaaacgtgct 1140
ggcgctgtg tgcgtaccgcaaa ggacaaggct cgcaagtctc gccgtatcag ccttgagtgc 1200
atgcttgagc aagccaataa gtttgctaac cataaggccg tctggttccc ttacaacatg 1260
gactggcgcg gtcgtgttca cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc 1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcgta aggaaggtaa ctactggctg 1380
aaaatccacg gtgcaaactg tgccgggtgtc gataaggttc cgccccgtga ggcgtatcaag 1440
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tggggctgtc agcaagatgc tccggcttcg ttccttgcgt tctgcttgcgt gtaacgtggg 1560
gtacagcacc acggcctgag ctataactgc tccctccgc tggcggttgc cgggtcttgc 1620
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tccaaagagt tcggcttcg tcaacaagtg ctggaaggta ccattcagcc agctattgt 1980
tccggcaagg gtctgatgtt cactcagccg aatcaggctg ctggatacat ggctaaactg 2040
atttggaaat ctgtgagcgt gacgggtgta gctgcgggtt aagcaatgaa ctggcttacg 2100
tctgctgtca agctgctggc tgctgaggctc aaagataaga agactggaga gattttcgc 2160
aagcgttgcg ctgtgcattt ggttaactctt gatggttcc cttatgtggca ggaatacaag 2220
aaggcttattc agacgcgcctt gaacctgtatg ttctcggtc agtccgcctt acaggctacc 2280
attaacacca acaaagatag cgagattgtt gcacacaaac aggagtctgg tatcgcttcc 2340
aactttgtac acagccaaga cggtagccac cttcgtaaga ctgttagtgc ggcacacgag 2400
aagtacggaa tcgaatcttt tgcaactgatt cacgactctc tcggtagccat tccggctgc 2460
gctgcgaacc tggtcaaaagc agtgcgcgaa actatggttt acacatatgc gtcttgcgt 2520
gtactggctgtt atttctacga ccgatgttcgat gaccagggttgc acgagctca attggacaaa 2580
atgccagcac ttccggctaa aggttaacttg aacctccgtg acatcttgcgt gtcggacttc 2640
gcgttcgctgaa 2652

<210> SEQ ID NO 48
<211> LENGTH: 883
<212> TYPE: PRT
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 48

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1				5					10					15	

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu

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20	25	30
Ala Arg Glu Gln Leu Ala Leu Glu His	Glu Ser Tyr	Glu Met Gly Glu
35	40	45
Ala Arg Phe Arg Lys Met	Phe Glu Arg Gln Leu Lys	Ala Gly Glu Val
50	55	60
Ala Asp Asn Ala Ala Ala	Lys Pro Leu Ile Thr	Thr Leu Leu Pro Lys
65	70	75
Met Ile Ala Arg Ile Asn Asp Trp	Phe Glu Glu Val Lys	Ala Lys Arg
85	90	95
Gly Lys Arg Pro Thr Ala Phe Gln	Phe Leu Gln Glu Ile Lys	Pro Glu
100	105	110
Ala Val Ala Tyr Ile Thr Ile Lys	Thr Leu Ala Cys	Leu Thr Ser
115	120	125
Ala Asp Asn Thr Thr Val Gln	Ala Val Ala Ser Ala	Ile Gly Arg Ala
130	135	140
Ile Glu Asp Glu Ala Arg Phe	Gly Arg Ile Arg Asp	Leu Glu Ala Lys
145	150	155
His Phe Lys Lys Asn Val Glu	Gln Leu Asn Lys	Arg Val Gly His
165	170	175
Val Tyr Lys Lys Ala Phe Met	Gln Val Val Glu Ala Asp	Met Leu Ser
180	185	190
Lys Gly Leu Leu Gly Gly	Glu Ala Trp Ser Ser	Trp His Lys Glu Asp
195	200	205
Ser Ile His Val Gly Val Arg	Cys Ile Glu Met	Leu Ile Glu Ser Thr
210	215	220
Gly Met Val Ser Leu His Arg	Gln Asn Ala Gly	Val Val Gly Gln Asp
225	230	235
Ser Glu Thr Ile Glu Leu Ala Pro	Glu Tyr Ala Glu Ala	Ile Ala Thr
245	250	255
Arg Ala Gly Ala Leu Ala Gly	Ile Ser Pro Met Phe	Gln Pro Cys Val
260	265	270
Val Pro Pro Lys Pro Trp Thr	Gly Ile Thr Gly Gly	Tyr Trp Ala
275	280	285
Asn Gly Arg Arg Pro Leu Ala Leu Val Arg	Thr His Ser Lys	Lys Ala
290	295	300
Leu Met Arg Tyr Glu Asp Val	Tyr Met Pro Glu Val	Tyr Lys Ala Ile
305	310	315
Asn Ile Ala Gln Asn Thr Ala Trp	Lys Ile Asn Lys	Lys Val Leu Ala
325	330	335
Val Ala Asn Val Ile Thr Lys	Trp Lys His Cys	Pro Val Glu Asp Ile
340	345	350
Pro Ala Ile Glu Arg Glu Leu	Pro Met Lys Pro Glu Asp	Ile Asp
355	360	365
Met Asn Pro Glu Ala Leu Thr	Ala Trp Lys Arg	Ala Ala Ala Val
370	375	380
Tyr Arg Lys Asp Lys Ala Arg	Lys Ser Arg Arg	Ile Ser Leu Glu Phe
385	390	395
Met Leu Glu Gln Ala Asn Lys	Phe Ala Asn His	Lys Ala Val Trp Phe
405	410	415
Pro Tyr Asn Met Asp Trp Arg	Gly Arg Val Tyr Ala Val	Ser Met Phe
420	425	430
Asn Pro Gln Gly Asn Asp Met	Thr Lys Gly Leu	Leu Thr Leu Ala Lys
435	440	445

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Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp
725 730 735

Gln Glu Tyr Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

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Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg	Asp	Ile	Leu	Glu	Ser	Asp	Phe
865				870			875				880				

Ala Phe Ala

<210> SEQ_ID NO 49
<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 49

atgaacacga	ttaacatcgc	taagaacgac	ttctctgaca	tcgaactggc	tgctatcccg	60
ttcaaacatc	tggctgacca	ttacggtag	cgtttagtc	cgaaacagtt	ggcccttgag	120
catgagtctt	acgagatggg	tgaagcacgc	ttccgcaaga	tgttgagcg	tcaactaaa	180
getggtgagg	ttgcggataa	cgtgccgc	aaggctctca	tcactaccct	actccctaag	240
atgattgcac	gcatcaacga	ctggtttag	gaagtgaaag	ctaagcgccg	caagcgccc	300
acagccttcc	agttctgca	agaaatcaag	ccggaaagccg	tagcgtacat	caccattaag	360
accactctgg	tttgcataac	cagtgcgtac	aatacaaccg	ttcaggctgt	agcaagcgca	420
atcggtcggg	ccatttgagga	cgaggctcgc	ttcggtcgta	tccgtgacct	tgaagctaa	480
cacttcaaga	aaaacgttga	ggaacaactc	aacaagcgccg	tagggcacgt	ctacaagaaa	540
gcatttatgc	aatgttgcga	ggctgacatg	ctctctaagg	gtctactcg	tggcgaggcg	600
tggcttcgt	ggcataagga	agactctatt	catgttaggag	tacgctgcat	cgagatgctc	660
attgagtcaa	ccggaatgg	tagtttacac	cgccaaaatg	ctggcgtagt	aggtaagac	720
tctgagacta	tcgaactcgc	acctgaatac	gctgaggcta	tgcaccccg	tgcaggtgc	780
ctggctggca	tctctccat	gttccaaact	tgcgttagtc	ctccctaagcc	gtggactggc	840
attactggtg	gtggctattt	ggcttaacgg	cgtcgcttc	tggcgcttgt	gcgtactcac	900
agtaagaag	cactgatgcg	ctacaaagac	gtttacatgc	ctgagggtgt	caaagcgatt	960
aacattgcgc	aaaacaccgc	atggaaaatc	aacaagaaag	tcctagcggt	cgccaaacgta	1020
atcacaagg	ggaaggattt	tccggtcgag	gacatccctc	cgattgagcg	tgaagaactc	1080
ccgatgaaac	cggaagacat	cgacatgaat	cctgaggctc	tcaccgcgt	gaaacgtgct	1140
gccgctgctg	tgtaccgaa	ggacaaggct	cgcgaatctc	gcccgtatcg	ccttgaggtt	1200
atgcttgagc	aagccaataa	gtttgctaac	cataaggccg	tctggttccc	ttacaacatg	1260
gactggcg	gtcggttta	cgtcggtca	atgttcaacc	cgcaaggtaa	cgatgtacc	1320
aaaggactgc	ttacgctggc	gaaaggtaaa	ccaatcggt	aggaaggta	ctactggctg	1380
aaaatccacg	gtgcaaaactg	tgccgggtgtc	gataaggttc	cgttccctga	gcccgtatcg	1440
ttcattgagg	aaaaccacga	gaacatcatg	gcttgcgtca	agtctccact	ggagaacact	1500
tgggtggctg	agcaagattt	tccgttctgc	ttccttgcgt	tctgcttgc	gtacgctgg	1560
gtacagcacc	acggcctgag	ctataactgc	tcccttccgc	tggcggttgc	cgggtcttgc	1620
tctggcatcc	agcacttctc	cgcgtatgc	cgagatgagg	taggtggctg	cgcggtaac	1680
ttgcttcaat	gtgaaaccgt	tcaggacatc	tacgggattt	ttgcttgcgt	gtacgctgg	1740
attctacaag	cagacgcaat	caatgggacc	gataacgaag	tagttaccgt	gaccgtatgg	1800
aacactgggt	aatctctga	gaaaggtaag	ctgggcacta	aggcactggc	tggtaatgg	1860
ctggcttacg	gtgttactcg	cagtgtgact	aagcggttgc	tcatgacgt	ggcttacggg	1920
tccaaagagt	tcggcttccg	tcaacaagtg	ctggaagata	ccattcagcc	agctatttgat	1980

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tccggcaagg	gtctgatgtt	cactcagccg	aatcaggctg	ctggatacat	ggctaagctg	2040
atttggaaat	ctgtgagcgt	gacgggtggta	gctgcggttt	aagcaatgaa	cgggcttaag	2100
tctgctgcta	agctgctggc	tgctgaggtc	aaagataaga	agactggaga	gattcttcgc	2160
aagcggtcg	ctgtgcattt	ggtaactctt	gatggttcc	ctatgtggca	ggaataacaag	2220
aagcctattc	agacgcgcgtt	gaacctgatg	ttcctcggtc	agttccgctt	acagectacc	2280
attaacacca	acaaagatag	cgagattgtat	gcacacaac	aggagtctgg	tatcgctcct	2340
aactttgtac	acagccaaga	cggtagccac	cttcgttaaga	ctgttagtgtg	ggcacacagag	2400
aagtacggaa	tcgaatcttt	tgcactgatt	cacgactctt	tccggtaccat	tccggctgac	2460
gctgcgaacc	tgttcaaagc	agtgcgcgaa	actatggttt	acacatatga	gtcttgtgat	2520
gtactggctg	atttctacga	ccagttcgct	gaccagtgc	acgagtctca	attggacaaa	2580
atgccagcac	ttccggctaa	aggtaacttg	aacctccgtg	acatcttaga	gtcggacttc	2640
gcgttcgcgt	aa					2652

<210> SEQ_ID NO 50

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 50

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1				5			10						15		

Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu
				20			25						30		

Ala	Arg	Glu	Gln	Leu	Ala	Leu	Glu	His	Glu	Ser	Tyr	Glu	Met	Gly	Glu
	35				40							45			

Ala	Arg	Phe	Arg	Lys	Met	Phe	Glu	Arg	Gln	Leu	Lys	Ala	Gly	Glu	Val
	50				55					60					

Ala	Asp	Asn	Ala	Ala	Lys	Pro	Leu	Ile	Thr	Thr	Leu	Leu	Pro	Lys	
65					70			75					80		

Met	Ile	Ala	Arg	Ile	Asn	Asp	Trp	Phe	Glu	Glu	Val	Lys	Ala	Lys	Arg
	85						90					95			

Gly	Lys	Arg	Pro	Thr	Ala	Phe	Gln	Phe	Leu	Gln	Glu	Ile	Lys	Pro	Glu
	100					105						110			

Ala	Val	Ala	Tyr	Ile	Thr	Ile	Lys	Thr	Leu	Ala	Cys	Leu	Thr	Ser	
	115					120					125				

Ala	Asp	Asn	Thr	Thr	Val	Gln	Ala	Val	Ala	Ser	Ala	Ile	Gly	Arg	Ala
	130				135					140					

Ile	Glu	Asp	Glu	Ala	Arg	Phe	Gly	Arg	Ile	Arg	Asp	Leu	Glu	Ala	Lys
145					150				155			160			

His	Phe	Lys	Lys	Asn	Val	Glu	Glu	Gln	Leu	Asn	Lys	Arg	Val	Gly	His
	165					170					175				

Val	Tyr	Lys	Lys	Ala	Phe	Met	Gln	Val	Val	Glu	Ala	Asp	Met	Leu	Ser
	180				185					190					

Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp	Ser	Ser	Trp	His	Lys	Glu	Asp
	195				200						205				

Ser	Ile	His	Val	Gly	Val	Arg	Cys	Ile	Glu	Met	Leu	Ile	Glu	Ser	Thr
	210				215			220							

Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn	Ala	Gly	Val	Val	Gly	Gln	Asp
225					230				235			240			

Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro	Glu	Tyr	Ala	Glu	Ala	Ile	Ala	Thr
	245				250				255			255			

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Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe
405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

200

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Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> SEQ ID NO 51

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 51

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catgagtctt	acgagatggg tgaagcacgc	ttccgcaaga tgtttgagcg	180
gctgggtagg	ttgcggataa cgctgccccc	aagcctctca tcactaccct	240
atgattgcac	gcatcaacga ctggtttgag	gaagtgaaag ctaagcgccg	300
acagccttcc	agttcctgca agaaatcaag	ccggaagccg tagcgtacat	360
accactctgg	ttgcctaact cagtgctgac	aataacaaccg ttcaaggctgt agcaagcgca	420
atcgggtcg	ccatttggg cgaggctcg	ttcggctcgta tccgtgacct	480
cacttcaaga	aaaacgttga ggaacaactc	aacaagcgccg tagggcacgt	540
gcatttatgc	aagttgtcg	ggctgacatg ctctctaagg gtctactcg	600
tggcttcgt	ggcataagga agactctatt	catgttaggg tacgctgcat	660
attgagtcaa	ccggaatgg	ctggtacac cgccaaatg ctggcgtagt	720
tctgagacta	tgcgaaactcg	acctaatac gctgaggcta	780
ctggctggca	tctctccgat	gttccaacct tgcgttagtt	840
attactggtg	gtggctattg ggctaacgg	cgtcgctc	900

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agtaagaaaag cactgatgcg ctacgaagac gtttacatgc ctgagggtgt acaaagcatt	960
aacattgcgc aaaacacccgc atggaaaatc aacaagaaaatc tccctagcggt cgccaacgtt	1020
atcaccaagt ggaaggcattt tccggtcgag gacatccctg cgattgagcg tgaagaactc	1080
ccgatgaaac cggaaagacat cgacatgaat cctgaggctc tcaccgcgtg gaaacgtgct	1140
gccgctgctg tggatccgaa ggacaaggct cgcaagtctc gccgtatcag ccttgaggcc	1200
atgcgttgcg aagccataa gtttgcatac cataaggccat tctgggtccc ttacaacatg	1260
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc	1320
aaaggactgc ttacgcgttgc gaaaggtaaa ccaatcggtt aggaaggtaa ctactggctg	1380
aaaatccacg gtgcaaaactg tgccgggtgtc gataaggttc cgttccctga ggcgcataag	1440
tccattgagg aaaaccacga gaacatcatg gcttgcgtca agtctccact ggagaacact	1500
tgggtggctg agcaagattc tccgttctgc ttcccttgcgt tctgcttga gtacgctggg	1560
gtacagcacc acggccttagt ctataactgc tcccttccgc tggcggttga cgggtctgc	1620
tctggcatcc agcacttctc cgcgatgttc cgagatgagg taggtggctcg cgccgttaac	1680
ttgcttccta gtgaaaccgt tcaggacatc tacgggattt tggcttaagaa agtcaacag	1740
attctacaag cagacgcaat caatgggacc gataacgaa tagttaccgt gaccgatgag	1800
aacactggtg aaatctctga gaaagtcaag ctgggcacta aggcactggc tggtaatgg	1860
ctggcttacg gtgttactcg cagtgactt aagcggttcg tcatgacgct ggcttacggg	1920
tccaaagagt tcggcttccg tcaacaagtg ctggaaaggta ccattcagcc agctattgat	1980
tccggcaagg gtctgatgtt cactcagccg aatcaggctg ctggatacat ggctaaagctg	2040
atttggaaat ctgtgagcgt gacgggtgtt gctgcgggtt aagcaatgaa cgggcttaag	2100
tctgctgtca agctgctggc tgctgaggctc aaagataaga agactggaga gattttcgc	2160
aagcggtgcg ctgtgcattt ggtaactctt gatggttcc ctatgtggca ggaataacaag	2220
aaggccttccg agacgcgcgtt gaacctgtat tccctcggtc agttccgtt acagcctacc	2280
attaacacca acaaagatag cgagattgtat gcacacaaac aggagtctgg tatcgctcct	2340
aactttgtac acagccaaaga cggttagccat cttcgttgcgat ctgtgtgtt ggcacacgag	2400
aagtacggaa tcgaatcttt tgcactgtt caccgttccat tccggctgac	2460
gtgtcgaaacc tggtaaaatc agtgcgcgaa actatgggtt acacatatga gtcttgcgt	2520
gtactggctg atttctacga ccagttcgat gaccagttgc acgagtctca attggacaaa	2580
atgccagcac ttccggctaa aggttaacttg aacctccgtg acatcttgcgtt gtcggacttc	2640
gegttcgcgt aa	2652

<210> SEQ ID NO 52

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 52

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu			
1	5	10	15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu			
20	25	30	

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu			
35	40	45	

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val			
50	55	60	

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Ala Asp Asn Ala Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
 65 70 75 80
 Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
 85 90 95
 Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
 100 105 110
 Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
 115 120 125
 Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
 130 135 140
 Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 145 150 155 160
 His Phe Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
 165 170 175
 Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 180 185 190
 Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 195 200 205
 Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 210 215 220
 Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 225 230 235 240
 Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
 245 250 255
 Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
 260 265 270
 Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
 275 280 285
 Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
 290 295 300
 Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
 305 310 315 320
 Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 325 330 335
 Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 340 345 350
 Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 355 360 365
 Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Val
 370 375 380
 Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400
 Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe
 405 410 415
 Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430
 Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445
 Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
 450 455 460
 Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
 465 470 475 480

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Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

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<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 53

atgaacacga ttaacatcgc taagaacgac ttctctgaca tcgaactggc tgctatcccg      60
ttcaacactc tggctgacca ttacggtag cgtttagtc gogaacagt ggcccttgag      120
catgagtctt acgagatggg tgaagcaacgc ttccgcaaga tgtttgagcg tcaacttaaa      180
gttggtgagg ttgcggataa cgctgcccgc aagcctctca tcactaccct actccctaag      240
atgattgcac acatcaacga ctgggtttag gaagtgaaag ctaagegcgg caagcgcgg      300
acagccttcc agttcctgca agaaatcaag ccggaagccg tagcgtacat caccattaag      360
accactctgg ctgccttaac cagtgctgac aataacaaccg ttcaaggctgt agcaagcgc      420
atcggctggg ccattgagga cgaggctcgc ttccggctgta tccgtgacct tgaagctaa      480
cacttcaaga aaaacgttga ggaacaactc aacaagcgcg tagggcacgt ctacaagaaa      540
gcattttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcgg tggcgaggcg      600
tggcttcgtt ggcataagga agactctatt catgttaggg tacgctgcat cgagatgctc      660
attgagtcaa ccggaatggg tagcttacac cgccaaaatg ctggcgttagt aggtcaagac      720
tctgagacta tcgaactcgc acctgaatac gctgaggctc tcgcaacccg tgcaggctcg      780
ctggctggca tctctccgat gttccaaacct tgcgttagttc ctccctaagcc gtggacttgc      840
attactgggt gtggctattt ggctaacggg cgtcgcttcc tggcgcttgt gcgtactcac      900
agtaagaaag cactgatgcg ctacgaagac gtttacatgc ctgagggtta caaagcgtt      960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tcctagcggg cgccaacgta     1020
atcacaagaatg ggaagcattt tccggctcgag gacatccctg cgattgagcg tgaagaactc     1080
ccgatgaaac ccggaaagacat cgacatgaat cctgaggctc tcaccgcgt gaaacgtgt     1140
gccgctgctg tgtaccgcaa ggacaaggct cgcaagtctc gccgtatcag ctttgaggct     1200
atgctttagc aagccaataa gtttgcatac cataaggccg tctggttccc ttacaacatg     1260
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatgtgacc     1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggtt aggaaggtaa ctactggctg     1380
aaaatccacg gtgcaaaactg tgccgggtgtc gataagggtt cgttccctga gcgcatcaag     1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgtca agtctccact ggagaacact     1500
tggctggctg agcaagattt tccgttctgc ttcccttgcgt tctgcttgcgt gtaacgtggg     1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcggttgc cgggtctgc     1620
tctggcatcc agcacttctc cgccatgtctc cgagatgagg taggtggctg cgccgttaac     1680
ttgcttccca gtgaaaccgt tcaggacatc tacgggattt ttgcttaagaa agtcaacgag     1740
attctacaag cagacgcaat caatgggacc gataacgaa tagttaccgt gaccgtatgag     1800
aacactgggt aaatctctga gaaagtcaag ctgggcacta aggcaactggc tggtaatgg     1860
ctggcttacg gtgttactcg cagtgtgact aagcgttgc tcatgacgct ggcttacggg     1920
tccaaagagt tcggcttccg tcaacaagtg ctggaaaggta ccattcagcc agctattgat     1980
tccggcaagg gtctgtatgtt cactcagccg aatcaggctg ctggatacat ggcttaagctg     2040
atttggaaat ctgtgagcgt gacgggtgtt gctgcgggtt aagcaatgaa cgggtttaag     2100
tctgctgcta agctgctggc tgctgaggctc aaagataaga agactggaga gattcttcgc     2160
aagcgttgcg ctgtgcattt ggttaactctt gatggttcc ctgtgtggca ggaatacaag     2220

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aaggcctattc agacgcgctt gaacctgatg ttcctcggtc agttccgctt acaggctacc 2280
attaacacca acaaagatag cgagattgat gcacacaac aggagtctgg tatcgctcct 2340
aactttgtac acagccaaga cggtagccac ctgcgtaaaga ctgttagtgg ggcacacgag 2400
aagtacggaa tcgaatctt tgcaactgatt cacgactcct tcggtaccat tcggctgac 2460
gtgcgaacc tggtaaaagc agtgcgcgaa actatggttg acacatatga gtcttgat 2520
gtactggctg atttctacga ccagttcgtc gaccagttgc acgagtctca attggacaaa 2580
atgccagcac ttccggctaa aggtaacttg aacccctccgtg acatctttaga gtcggacttc 2640
gcgttcgcgt aa 2652

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<210> SEQ ID NO 54
<211> LENGTH: 883
<212> TYPE: PRT
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 54

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Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
1 5 10 15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
20 25 30

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
35 40 45

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
50 55 60

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
65 70 75 80

Met Ile Ala His Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
85 90 95

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
100 105 110

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
115 120 125

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
130 135 140

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
145 150 155 160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
165 170 175

Val Tyr Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
275 280 285

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Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
 290 295 300
 Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
 305 310 315 320
 Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 325 330 335
 Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 340 345 350
 Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 355 360 365
 Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
 370 375 380
 Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400
 Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe
 405 410 415
 Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430
 Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445
 Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
 450 455 460
 Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
 465 470 475 480
 Phe Ile Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
 485 490 495
 Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
 500 505 510
 Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
 515 520 525
 Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
 530 535 540
 His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Arg Ala Val Asn
 545 550 555 560
 Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
 565 570 575
 Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
 580 585 590
 Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
 595 600 605
 Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
 610 615 620
 Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
 625 630 635 640
 Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln
 645 650 655
 Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg

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705	710	715	720
Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp			
725	730	735	
Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu			
740	745	750	
Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu			
755	760	765	
Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His			
770	775	780	
Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu			
785	790	795	800
Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr			
805	810	815	
Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met			
820	825	830	
Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln			
835	840	845	
Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu			
850	855	860	
Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe			
865	870	875	880

<210> SEQ ID NO 55
<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 55
atgaacacga ttaacatcgcaagaacgacttctgaca tgcggactggc tgctatcccg 60
ttcaaacactctggctgacca ttacggtagcggttagctc ggcggacagtt ggcctttag 120
catgagtctt acggatgggtgaagcacgc ttccgcaaga tggttagcgctcaacttaaa 180
gctggtaggg ttgcggataa cgctgcgc aaggctctca tcaactaccct actccctaag 240
atgattgcac acatcaacga ctgggttag gaagtggaaag ctaaggcgccg caaggccccg 300
acagccttc agttctgca agaaaatcaag ccggaaagccg tagcgtacat caccattaag 360
accactctgg cttgcctaaac cagtgctgac aatacaaccg ttcaggctgt agcaagcgca 420
atcggtcgccg ccattggagga cgaggctcgcttcgggtcgta tccgtgaccc tgaagctaa 480
cacttcaaga aaaacgttga ggaacaactc aacaaggcgccg tagggcacgt ctacaagaaa 540
gcatttatgc aagttgtcga ggctgacatcgctctcaagg gtctactcggtggcgaggcg 600
tggtcttcgt ggcataagga agactctatt catgttaggat tacgctgcat cgagatgctc 660
attgagtcaa cggaaatggtagttacac cgccaaatcg tggcgctgt aggtcaagac 720
tctgagacta tcgaactcgacctgaatacgctgaggctatcgcaaccctgcaggctgcg 780
ctggctggca tctctccgat gttccaaacct tgcgttagttc tccctaaagcc gtggactggc 840
attactggtg gtggcttattggctaacggctgtcgctc tggcgctggcgtactc 900
agtaagaaag cactgatgcg ctacgaagac gtttacatgc ctgaggctgttgcggatt 960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tccctagcggt cgccaaacgtaa 1020
atcaccaagt ggaaggatgttccggctcgag gacatccctcgatcgattgacgctgaagaactc 1080
ccqatqaac cqqaqqacat cqacatqaat cctqaqqctctacccqctq qaaacqgtqct 1140

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gccgctgctg tgtaccccaa ggacaaggct cgcaagtctc gccgtatcatc ccttgagttc 1200
atgcgttgcg aagccaataa gtttgcatac cataaggccc tctgggtccc ttacaacatg 1260
gactggcgcg gtcgtgtta cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc 1320
aaaggactgc ttacgtggc gaaaggtaaa ccaatcggtt aggaagggtt ctactggctg 1380
aaaatccacg gtgcaaactg tgccgggtgtc gataagggtt cgttccctga gcgcatacg 1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgtca agtctccact ggagaacact 1500
tggtggctg agcaagattc tccgttctgc ttccttgcgt tctgtttga gtacgctgg 1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcggttga cgggtcttgc 1620
tctggcatcc agcacttctc cgcgatgtctc cgagatgagg taggtggctg cgcggttaac 1680
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aacactgggt aaatctctga gaaagtcaag ctgggcacta aggcaactggc tggtaatgg 1860
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tccaaagagt tcgggttccg tcaacaagtgc ctggaaaggta ccattcagcc agtatttgat 1980
tccggcaagg gtctgtatgtt cactcagccg aatcagggttgc ctggatacat ggcttaagctg 2040
atttggaaat ctgtgagcgt gacgggtggta gctgcgggtt aagcaatgaa ctgggttaag 2100
tctgctgcta agctgctggc tgctgaggctc aaagataaga agactggaga gattttcgc 2160
aagcggttgcg ctgtgcattt ggttaactctt gatggttcc ctatgtggca ggaataacaag 2220
aagcctattt agacgcgtt gaaacctgtt ttcctcggtc agttccgtt acagectacc 2280
attaacacca acaaagatag cgagatgttgc gcacacaaac aggagtctgg tatacgctt 2340
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aagtacggaa tcgaatcttt tgcaactgattt cacgactctt tccggctgac 2460
gtctgcgaaacc tggtaaaggc agtgcgcgaa actatgggtt acacatatga gtctgtgat 2520
gtactggctg atttctacga ccagttcgtt gaccgttgc acgagtctca attggacaaa 2580
atgccagcac ttccggctaa aggttaacttg aacctccgtt acatctttaga gtccggacttc 2640
gcgttgcgtt aa 2652

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<210> SEQ ID NO 56

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 56

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1								10					15		

Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu
													30		
20								25							

Ala	Arg	Glu	Gln	Leu	Ala	Leu	Glu	His	Glu	Ser	Tyr	Glu	Met	Gly	Glu
													35		
													40		

Ala	Arg	Phe	Arg	Lys	Met	Phe	Glu	Arg	Gln	Leu	Lys	Ala	Gly	Glu	Val
												50			55
												55			60

Ala	Asp	Asn	Ala	Ala	Lys	Pro	Leu	Ile	Thr	Thr	Leu	Leu	Pro	Lys
65													80	

Met	Ile	Ala	His	Ile	Asn	Asp	Trp	Phe	Glu	Glu	Val	Lys	Ala	Lys	Arg
												85			90
												90			95

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Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
100 105 110

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
115 120 125

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
130 135 140

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
145 150 155 160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
165 170 175

Val Tyr Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe
405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr

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515	520	525
Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln		
530	535	540
His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn		
545	550	555
Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys		
565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn		
580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys		
595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly		
610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly		
625	630	635
Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln		
645	650	655
Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln		
660	665	670
Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr		
675	680	685
Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys		
690	695	700
Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg		
705	710	715
Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp		
725	730	735
Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu		
740	745	750
Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu		
755	760	765
Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His		
770	775	780
Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu		
785	790	795
Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr		
805	810	815
Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met		
820	825	830
Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln		
835	840	845
Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu		
850	855	860
Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe		
865	870	875
Ala Phe Ala		

<210> SEQ ID NO 57

<211> LENGTH: 2652

<212> TYPE: DNA

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 57

atgaacacgtaaacatcgcttaagaacgacttctctgacatcgaactggctgcttatcccc 60

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ttcaacactc tggctgacca ttacggtag cgtttagctc gcgaaacagt ggcccttgag	120
catgagtctt acgagatggg tgaaggcacgc ttccgcaaga tgtttggcg tcaacttaaa	180
gctggtgagg ttgcggataa cgctgccgc aagcctctca tcactaccct actccctaag	240
atgattgcac acatcaacga ctgggtttag gaaatgaaaag ctaagcgccg caagcgccc	300
acagccttcc agttctgca agaaatcaag ccggaagccg tagcgtacat caccattaag	360
accactctgg ttgctctaact cagtgctgac aatacaaccg ttccaggctgt agcaagcgca	420
atcggtcggtt ccattgagga cgaggctcg ttcggctgta tccgtgacct tgaagctaag	480
cacttcaaga aaaacgttga ggaacaactc aacaagcgcc tagggcacgt ctacaagaaa	540
gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcgg tggcgaggcg	600
tggcttcgtt ggcataagga agactctatt catgttaggag tacgctgcat cgagatgtc	660
attgagtcaa ccggaaatggg tagcttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcgc acctgaatac gctgaggota tgcgaacccg tgcaggtgcg	780
ctggctggca tctctccgat gttccaaccc tgcgttagttc ctccctaagcc gtggactggc	840
attactgggt gtggctattt ggctaacggg cgtcgctcctc tggcgctgggt gcgtactcac	900
agtaagaaaag cactgtatgcg ctacgaagac gtttacatgc ctgagggtta caaagcgatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaaag tccctagcggt cgccaaacgta	1020
atcaccaagt ggaaggatttgc tccggctcgag gacatccctg cgattgagcg tgaagaactc	1080
ccgatgaaac ccggaaagacat cgacatgaat cctgaggctc tcaccggctg gaaacgtgct	1140
gccgctgctg tgtaccgcaa ggacaaggct cgcaagtctc ggcgtatcag cttgaggattc	1200
atgcttgcgc aagccataaa gtttgcatac cataaggccg tctgggttcc ttacaacatg	1260
gactggcgcg gtctgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc	1320
aaaggactgc ttacgctggc gaaaggtaaa ccaatcggttta aggaaggtaa ctactggctg	1380
aaaatccacg gtgcaactg tgccgggtgtc gataagggttcc cgttccctga ggcgcataag	1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgtca agtctccact ggagaacact	1500
tggggctgt agcaagatttgc tccgttctgc ttccctgctgt tctgcttga gtacgctggg	1560
gtacagcacc acggctgtgag ctataactgc tcccttccgc tggcggttga cgggtctgc	1620
tctggcatcc agcacttctc cgcgatgtc cgagatgagg taggtggctcg cgccgttaac	1680
ttgcttctca gtgaaaccgt tcaggacatc tacgggatgtt tggctaaagaa agtcaacgag	1740
attctacaag cagacgcaat caatgggacc gataacgaag tagttaccgt gaccgatgag	1800
aacactgggtt aatctctga gaaatgtcaag ctgggcacta aggcaactggc tggtaatgg	1860
ctggcttacg gtgttactcg cagtgactt aagcggttccatcg tcatgacgct ggcttacggg	1920
tccaaagagt tcggcttccg tcaacaactg ctggaaagata ccattcagcc agtattgtat	1980
tccggcaagg gtctgtatgtt cactcagccg aatcaggctg ctggatacat ggctaaactg	2040
atttggaaat ctgtgagcgt gacgggtggta gctgcgggtt aagcaatgaa cgggtttaag	2100
tctgctgtca agctgtgtgc tgctgtgtca aaagataaga agactggaga gattttcg	2160
aagcggttgcg ctgtgttccg ggttaacttcc gatgggttcc ctatgtggca ggaatacaag	2220
aaggccatttc agacgcgtt gaaacctgtatg ttccctgggttcc agttcccgctt acagcctacc	2280
attaacacca acaaagatag cgagattgtatg gcacacaaac aggagttctgg tatcgctcct	2340
aactttgtac acagccaaga cggttagccac ctgcgtttaa ctgtgtgtt ggcacacgag	2400

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aagtacggaa tcgaatctt tgcactgatt cacgactcct tcggtaaccat tccggctgac	2460
gctgcgaacc tggtcaaggc agtgcgcgaa actatggttt acacatatga gtcttgat	2520
gtactggctg atttctacga ccagttcgct gaccagttgc acgagtctca attggacaaa	2580
atgccagcac ttccggctaa aggtaacttg aacctccgtg acatcttaga gtcggacttc	2640
gcgttcgcgt aa	2652

<210> SEQ ID NO 58

<211> LENGTH: 883

<212> TYPE: PRT

<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 58

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu			
1	5	10	15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu			
20	25	30	

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu			
35	40	45	

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val			
50	55	60	

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys			
65	70	75	80

Met Ile Ala His Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg			
85	90	95	

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu			
100	105	110	

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser			
115	120	125	

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala			
130	135	140	

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys			
145	150	155	160

His Phe Lys Lys Asn Val Glu Gln Leu Asn Lys Arg Val Gly His			
165	170	175	

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser			
180	185	190	

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp			
195	200	205	

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr			
210	215	220	

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp			
225	230	235	240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr			
245	250	255	

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val			
260	265	270	

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Tyr Trp Ala			
275	280	285	

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala			
290	295	300	

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile			
305	310	315	320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala	
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228

325	330	335
Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile		
340	345	350
Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp		
355	360	365
Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val		
370	375	380
Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe		
385	390	395
400		
Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe		
405	410	415
Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe		
420	425	430
Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys		
435	440	445
Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly		
450	455	460
Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys		
465	470	475
480		
Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro		
485	490	495
Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu		
500	505	510
Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr		
515	520	525
Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln		
530	535	540
His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn		
545	550	555
560		
Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys		
565	570	575
Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn		
580	585	590
Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys		
595	600	605
Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly		
610	615	620
Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly		
625	630	635
640		
Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln		
645	650	655
Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln		
660	665	670
Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr		
675	680	685
Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys		
690	695	700
Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg		
705	710	715
720		
Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp		
725	730	735
Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu		
740	745	750

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aaaggactgc ttacgctggc gaaaggtaaa ccaatcggtt aggaagggtt ctactggctg 1380
aaaatccacg gtgcaaactg tgccgggtgtc gataagggtt cgttccctga gcgcattcaag 1440
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tggggcgtc agcaagattc tccgttctgc ttcccttgcgt tctgcgttga gtacgctgg 1560
gtacagcacc acggcctgag ctataactgc tcccttcgc tggcggttga cgggtctgc 1620
tctggcatcc agcacttctc cgccatgttc cgagatgagg taggtggtcg cgggttaac 1680
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tctgctgcta agctgctggc tgctgagggtc aaagataaga agactggaga gattttcgc 2160
aagcgttgcg ctgtgcattt ggttacttctt gatggttcc ctatgtggca ggaataacaag 2220
aagcctattt agacgcgcgtt gaaacctgtatg ttcctcggtt agttccgcgtt acagcctacc 2280
attaacacca acaaagatag cgagattgtatg gcacacaaac aggagtctgg tatcgctcct 2340
aactttgtac acagccaaga cggtagccac cttcgtaaga ctgttagtgg ggcacacgag 2400
aagtacggaa tcgaatcttt tgcaactgattt cacgactcct tcggtaccat tccggctgac 2460
gctgcgaacc tggtaaaagc agtgcgcgaa actatggttt acacatatga gtcttggat 2520
gtactggctt atttctacga ccagttcgctt gaccagttgc acgagtctca attggacaaa 2580
atgccagcac ttccggctaa aggttaacttg aacccctcggtt acatctttaga gtcggacttc 2640
gcgttgcgtt aa 2652

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<210> SEQ_ID NO 60
<211> LENGTH: 883
<212> TYPE: PRT
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 60

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Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
1 5 10 15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
20 25 30

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
35 40 45

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
50 55 60

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
65 70 75 80

Met Ile Ala His Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
85 90 95

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
100 105 110

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
115 120 125

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala

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130	135	140
Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys		
145	150	155
160		
His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His		
165	170	175
Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser		
180	185	190
Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp		
195	200	205
Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr		
210	215	220
Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp		
225	230	235
240		
Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr		
245	250	255
Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val		
260	265	270
Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala		
275	280	285
Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala		
290	295	300
Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile		
305	310	315
320		
Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala		
325	330	335
Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile		
340	345	350
Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp		
355	360	365
Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val		
370	375	380
Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe		
385	390	395
400		
Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe		
405	410	415
Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe		
420	425	430
Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys		
435	440	445
Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly		
450	455	460
Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys		
465	470	475
480		
Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro		
485	490	495
Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu		
500	505	510
Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr		
515	520	525
Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln		
530	535	540
His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn		
545	550	555
560		

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<210> SEQ ID NO 61
<211> LENGTH: 2652
<212> TYPE: DNA
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 61

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ttcaaacactc tggctgacca ttacggtgag cgtttagctc gcgaacagtt ggcctttag	120
catgagtctt acgagatggg tgaagcacgc ttccgcaga tgggtggcg tcaacttaaa	180
gctgggtgagg ttgcggataa cgctgcccgc aagcctctca tcaactaccct actccctaag	240

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atgattgcac acatcaacga ctggtttag gaagtgaaag ctaagcgccg caagegcccc	300
acagccttc agttoctgca agaaaatcaag ccggaagccg tagcgtacat caccattaag	360
accactctgg cttgectaac cagtgctgac aataacaaccg ttcaggctgt agcaagcgca	420
atcggctggg ccattgagga cgaggctcg ttcggctgta tccgtgacct tgaagctaa	480
cacttcaaga aaaacgttga ggaacaactc aacaagcgac tagggcacgt ctacaagaaa	540
gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcg tggcgaggcg	600
tggtcttcgt ggcataagga agactctatt catgttaggag tacgctgcat cgagatgtc	660
attgagtcaa cggaaatggt tagttacac cgccaaaatg ctggcgtagt aggtcaagac	720
tctgagacta tcgaactcg acctgaatac gctgaggctt tgcaccaaccg tgcagggtcg	780
ctggctggca tctctccgat gttccaacct tgcgttagtt ctcctaagcc gtggactggc	840
attactggtg gtggctattt ggctaacggt cgtcgtctc tggcgcttgtt gcgtactcac	900
agtaagaaag cactgatgac ctacgaagac gtttacatgc ctgagggtta caaagcgatt	960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaag tcctagcggt cgccaaacgta	1020
atcacaagg ggaagcattt tccggctcgag gacatccctg cgattgagcg tgaagaactc	1080
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atgcgttgcg aagcaataa gtttgcatac cataaggccg tctgggtccc ttacaacatg	1260
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gtacagcacc acggccctgag ctataactgc tcccttccgc tggcggttgc cgggtcttgc	1620
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tccaaagagt tcggcttccg tcaacaagtgc ctggaaaggta ccattcagcc agcttattgt	1980
tccggcaagg gtctgtatgtt cactcagccg aatcaggctg ctggatacat ggctaaagctg	2040
atttggaaat ctgtgagcgt gacgggttgc gctgcgggttgc aagcaatgaa cgggtttaag	2100
tctgctgtca agctgtgtgc tgctgagggtc aaagataaga agactggaga gattttcgc	2160
aagcggttgcg ctgtgcattt ggttaactctt gatggttccctt ctatgtggca ggaataacaag	2220
aagcctattt agacgcgtt gaaacctgtt ttcctcggtt agttccgtt acagcctacc	2280
attaacacca acaaagatag cgagattgtt gCACACAAAC aggagtctgg tatcgcttcc	2340
aactttgtac acagccaaga cggtagccac cttcgtttaa ctgtgtgtt ggcacacgag	2400
aagtacggaa tcgaatcttt tgcaactgtt cacgactctt tccggatcat tccggctgac	2460
gtgtgcgtacc tggtaaaggc agtgcgtccaa actatggttt acacatatga gtcttgcgt	2520
gtactggctg atttctacga ccagttcgtt gaccagggttgc acgagtctca attggacaaa	2580
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gcgttcgcgt aa 2652

<210> SEQ_ID NO 62
<211> LENGTH: 883
<212> TYPE: PRT
<213> ORGANISM: T7 bacteriophage

<400> SEQUENCE: 62

Met	Asn	Thr	Ile	Asn	Ile	Ala	Lys	Asn	Asp	Phe	Ser	Asp	Ile	Glu	Leu
1			5			10				15					
Ala	Ala	Ile	Pro	Phe	Asn	Thr	Leu	Ala	Asp	His	Tyr	Gly	Glu	Arg	Leu
	20			25			30								
Ala	Arg	Glu	Gln	Leu	Ala	Leu	Glu	His	Glu	Ser	Tyr	Glu	Met	Gly	Glu
	35			40			45								
Ala	Arg	Phe	Arg	Lys	Met	Phe	Glu	Arg	Gln	Leu	Lys	Ala	Gly	Glu	Val
	50			55			60								
Ala	Asp	Asn	Ala	Ala	Ala	Lys	Pro	Leu	Ile	Thr	Thr	Leu	Leu	Pro	Lys
65				70			75					80			
Met	Ile	Ala	His	Ile	Asn	Asp	Trp	Phe	Glu	Glu	Val	Lys	Ala	Lys	Arg
	85				90			95							
Gly	Lys	Arg	Pro	Thr	Ala	Phe	Gln	Phe	Leu	Gln	Glu	Ile	Lys	Pro	Glu
	100				105			110							
Ala	Val	Ala	Tyr	Ile	Thr	Ile	Lys	Thr	Leu	Ala	Cys	Leu	Thr	Ser	
	115				120			125							
Ala	Asp	Asn	Thr	Thr	Val	Gln	Ala	Val	Ala	Ser	Ala	Ile	Gly	Arg	Ala
	130				135			140							
Ile	Glu	Asp	Glu	Ala	Arg	Phe	Gly	Arg	Ile	Arg	Asp	Leu	Glu	Ala	Lys
145				150			155			160					
His	Phe	Lys	Lys	Asn	Val	Glu	Glu	Gln	Leu	Asn	Lys	Arg	Val	Gly	His
	165				170			175							
Val	Tyr	Lys	Ala	Phe	Met	Gln	Val	Val	Glu	Ala	Asp	Met	Leu	Ser	
	180				185			190							
Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp	Ser	Ser	Trp	His	Lys	Glu	Asp
	195				200			205							
Ser	Ile	His	Val	Gly	Val	Arg	Cys	Ile	Glu	Met	Leu	Ile	Glu	Ser	Thr
	210				215			220							
Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn	Ala	Gly	Val	Val	Gly	Gln	Asp
225				230			235			240					
Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro	Glu	Tyr	Ala	Glu	Ala	Ile	Ala	Thr
	245				250			255							
Arg	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser	Pro	Met	Phe	Gln	Pro	Cys	Val
	260				265			270							
Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile	Thr	Gly	Gly	Tyr	Trp	Ala	
	275				280			285							
Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val	Arg	Thr	His	Ser	Lys	Lys	Ala
	290				295			300							
Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met	Pro	Glu	Val	Tyr	Lys	Ala	Ile
305				310			315			320					
Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys	Ile	Asn	Lys	Lys	Val	Leu	Ala
	325				330			335							
Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys	His	Cys	Pro	Val	Glu	Asp	Ile
	340				345			350							
Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro	Met	Lys	Pro	Glu	Asp	Ile	Asp
	355				360			365							

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Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
 370 375 380
 Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400
 Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Val Trp Phe
 405 410 415
 Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430
 Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445
 Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
 450 455 460
 Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
 465 470 475 480
 Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
 485 490 495
 Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
 500 505 510
 Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
 515 520 525
 Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
 530 535 540
 His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
 545 550 555 560
 Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
 565 570 575
 Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
 580 585 590
 Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
 595 600 605
 Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
 610 615 620
 Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
 625 630 635 640
 Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Gly Thr Ile Gln
 645 650 655
 Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Gly Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
 705 710 715 720
 Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Met Trp
 725 730 735
 Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
 740 745 750
 Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
 755 760 765
 Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
 770 775 780

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Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> SEQ_ID NO 63

<211> LENGTH: 3075

<212> TYPE: DNA

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 63

atgaccatga ttacggattc actggccgtc gttttacaac gtcgtactg ggaaaacctt	60
ggcggttaccc aacttaatcg ccttcagca catccccctt tcgcccagctg gcgtaatagc	120
gaagaggccc gcaccgatcg cccttccaa cagttgcgca gcctaatgg cgaatggcgc	180
tttgccttgtt ttccggcacc agaagcggtg ccggaaagct ggctggagtg cgatcttct	240
gaggccgata ctgtcgtcgt cccctcaaac tggcagatgc acggttacga tgcccccattc	300
tacaccaacg tgacctatcc cattacggtc aatccggctt ttgttccac ggagaatccg	360
acgggttgtt actcgcgtcac atttaatgtt gatgaaagct ggctacagga aggccagacg	420
cgaattatcc ttgatggcgt taactcggcg tttcatctgt ggtgcaacgg gcgctgggtc	480
ggttacggcc aggacagtcg tttccgtct gaatttggacc tgagcgcatt tttacgcgcc	540
ggagaaaaacc gcctcgcgg gatggtgctg cgctggagtg acggcagttt tctggaaagat	600
caggatatgt ggccggatgag cggcattttc cgtgacgtct cgttgcgtca taaaccgact	660
acacaaatca gcgatttcca tggccact cgcttaatg atgattttag ccgcgtgtat	720
ctggaggctg aagttcagat gtgcggcgg ttcgtactt acctacgggt aacagttct	780
ttatggcagg gtgaaacgc ggtcgccagc ggcaccgcgc ctttcggccg tgaaattatc	840
gatgagcgtg gtggatatgc cgatcgcgtc acactacgtc tgaacgtcga aaacccgaaa	900
ctgtggagcg ccgaaatccc gaatcttat cgtgcgggtgg ttgaactgca caccggcgc	960
ggcacgcgtga ttgaaggcaga agcctcgtcat gtcgggttcc gcgagggtgcg gattgaaaat	1020
ggtctgtgc tgctgaacgg caagccgtt ctgattcggag gctttaaccg tcacgagcat	1080
catcctctgc atggcaggt catggatgag cagacgtatgg tgcaggatat cctgtgtat	1140
aagcagaaca actttaacgc cgtgcgtgt tcgcattatc cgaaccatcc gctgtggat	1200
acgctgtgcg accgcgtacgg cctgtatgtt gtggatggaa ccaatattga aacccacggc	1260
atggtgccaa tgaatcgtct gaccgtatgtt ccgcgtgtgc taccggcgtat gagcgtacgc	1320
gtaacgcgaa tggtgacgcg cgatcgtat caccggatgt tgatcatctg gtcgtgggg	1380
aatgaatcgtatgcgc taatcgtatgc ggcgtgtatc gtcggatcaa atctgtcgat	1440
ccttccgcgc cggcgtatgtt tgaaggcggc ggagccgaca ccacggccac cgatattatt	1500
tgcccgatgt acgcgtgcgtt ggtgaaagac cagcccttcc cggctgtgcc gaaatggtcc	1560

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atcaaaaaat ggctttcgct acctggagag acgcgccecg tgcgttgc cgaatacgcc 1620
cacgcgatgg gtaacagtct tggeggtttc gctaaatact ggcaggcggt tcgtcgttat 1680
ccccgtttac aggggggctt cgctggac tgggtggatc atgcgtgtat taaatatgt 1740
gaaaacggca acccggtggc ggcttacggc ggtgatttg gcgatacgcc gaacgatcgc 1800
cagttctgtt tgaacggctt ggtcttgcc gaccgcacgc cgcacccagc gctgacggaa 1860
gcaaaacacc agcagcagg tttccaggcc cgtttacggc ggcaaaccat cgaagtgcacc 1920
agcgaatacc tggccgtca tagcgataac gagtcctgc actggatggt ggcgtggat 1980
ggtaagccgc tggcaagcgg tgaagtgcct ctggatgtcg ctccacaagg taaacagtt 2040
attgaactgc ctgaactacc gcagccggag agcgccggc aactctggct cacagtcgc 2100
gtatgtcaac cgaacgcgac cgcattgtca gaagccggc acatcagcgc ctggcagcag 2160
tggcgtctgg cggaaaacct cagtgtgacg ctccccccgc cgtccacgc catccgcatt 2220
ctgaccacca gcgaaatgga tttttgcata gagctgggta ataagcgttg gcaatttaac 2280
cgccagtcag gcttttttc acagatgtgg attggcgata aaaaacaact gctgacgccc 2340
ctgcgcgatc agttcaccccg tgccacgcgt gataacgaca ttggcgtaag tgaagcgcacc 2400
cgcattgacc ctaacgcctg ggtcgaacgc tggaaaggcgg cggccattt ccagggcggaa 2460
gcagcgttgt tgcaagtgcac ggcagataca cttgctgtat cgggtgtat tacgaccgt 2520
cacgcgtggc agcatcaggg gaaaacctta tttatcagcc gggaaaacctt ccggattgtat 2580
ggtagtggtc aaatggcgat taccgttgc gttgaagtgg cgagcgatac accgcattccg 2640
gcgcggattt gcctgaactg ccagctggcg caggtagcag agcgggtaaa ctggctcgga 2700
ttaggggccgc aagaaaacta tcccgaccgc cttactgcgc cttgtttgttccgcgtggat 2760
ctgccattgt cagacatgtt taccggatc gtcttccgc gggaaaacgg tctggcgtgc 2820
gggacgcggc aattgtat tggccacac cagttggcgcc gggacttcca gttcaacatc 2880
agccgcgtaca gtcaacagca actgtatggaa accagccatc gccatctgttccgcgtggaa 2940
gaaggcgcata ggttgcataat cggatggatc cttatggggat tgggtggcgca cggacttccgg 3000
agcccgatcgtt cttatggcgat attccagctg agcgccggcgtt gttaccattt ccagttggc 3060
ttttgttcaaa aataaa 3075

<210> SEQ ID NO 64
<211> LENGTH: 1024
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 64

Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Arg Asp
1 5 10 15

Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro
20 25 30

Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro
35 40 45

50 55 60

65 70 75 80
 Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr

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Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile Thr Val Asn Pro
 100 105 110
 Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys Tyr Ser Leu Thr Phe
 115 120 125
 Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln Thr Arg Ile Ile Phe
 130 135 140
 Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys Asn Gly Arg Trp Val
 145 150 155 160
 Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu Phe Asp Leu Ser Ala
 165 170 175
 Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val Met Val Leu Arg Trp
 180 185 190
 Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met Trp Arg Met Ser Gly
 195 200 205
 Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro Thr Thr Gln Ile Ser
 210 215 220
 Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp Phe Ser Arg Ala Val
 225 230 235 240
 Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu Arg Asp Tyr Leu Arg
 245 250 255
 Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln Val Ala Ser Gly Thr
 260 265 270
 Ala Pro Phe Gly Glu Ile Ile Asp Glu Arg Gly Tyr Ala Asp
 275 280 285
 Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro Lys Leu Trp Ser Ala
 290 295 300
 Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu Leu His Thr Ala Asp
 305 310 315 320
 Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val Gly Phe Arg Glu Val
 325 330 335
 Arg Ile Glu Asn Gly Leu Leu Leu Asn Gly Lys Pro Leu Leu Ile
 340 345 350
 Arg Gly Val Asn Arg His Glu His His Pro Leu His Gly Gln Val Met
 355 360 365
 Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu Met Lys Gln Asn Asn
 370 375 380
 Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn His Pro Leu Trp Tyr
 385 390 395 400
 Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val Asp Glu Ala Asn Ile
 405 410 415
 Glu Thr His Gly Met Val Pro Met Asn Arg Leu Thr Asp Asp Pro Arg
 420 425 430
 Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg Met Val Gln Arg Asp
 435 440 445
 Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu Gly Asn Glu Ser Gly
 450 455 460
 His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp Ile Lys Ser Val Asp
 465 470 475 480
 Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Ala Asp Thr Thr Ala
 485 490 495
 Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val Asp Glu Asp Gln Pro
 500 505 510
 Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys Trp Leu Ser Leu Pro

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249**250**

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515

520

525

Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr Ala His Ala Met Gly
 530 535 540

Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln Ala Phe Arg Gln Tyr
 545 550 555 560

Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp Val Asp Gln Ser Leu
 565 570 575

Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser Ala Tyr Gly Gly Asp
 580 585 590

Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys Met Asn Gly Leu Val
 595 600 605

Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr Glu Ala Lys His Gln
 610 615 620

Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln Thr Ile Glu Val Thr
 625 630 635 640

Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu Leu Leu His Trp Met
 645 650 655

Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly Glu Val Pro Leu Asp
 660 665 670

Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu Pro Glu Leu Pro Gln
 675 680 685

Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val Arg Val Val Gln Pro
 690 695 700

Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile Ser Ala Trp Gln Gln
 705 710 715 720

Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu Pro Ala Ala Ser His
 725 730 735

Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp Phe Cys Ile Glu Leu
 740 745 750

Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser Gly Phe Leu Ser Gln
 755 760 765

Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr Pro Leu Arg Asp Gln
 770 775 780

Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly Val Ser Glu Ala Thr
 785 790 795 800

Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp Lys Ala Ala Gly His
 805 810 815

Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr Ala Asp Thr Leu Ala
 820 825 830

Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp Gln His Gln Gly Lys
 835 840 845

Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile Asp Gly Ser Gly Gln
 850 855 860

Met Ala Ile Thr Val Asp Val Glu Val Ala Ser Asp Thr Pro His Pro
 865 870 875 880

Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln Val Ala Glu Arg Val
 885 890 895

Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr Pro Asp Arg Leu Thr
 900 905 910

Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu Ser Asp Met Tyr Thr
 915 920 925

Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg Cys Gly Thr Arg Glu
 930 935 940

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Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp Phe Gln Phe Asn Ile
 945 950 955 960
 Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr Ser His Arg His Leu
 965 970 975
 Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile Asp Gly Phe His Met
 980 985 990
 Gly Ile Gly Asp Asp Ser Trp Ser Pro Ser Val Ser Ala Glu Phe
 995 1000 1005
 Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu Val Trp Cys Gln
 1010 1015 1020

Lys

<210> SEQ_ID NO 65
 <211> LENGTH: 3075
 <212> TYPE: DNA
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 65

atgactatga ttacagattc	actggccgtc	gttttacaac	gtcgtgactg	ggaaaacct	60	
ggcggttaccc	aacttaatcg	ccttgcagca	catccccctt	tgcgcagctg	gcgtaatagc	120
gaagaggccc	gcaccaatcg	cccttcccag	cagttgcgc	gcctgaatgg	tgagtggcaa	180
tttgtcttgtt	ttccggcacc	agaagcggtt	ccggaaagct	ggctggagtg	cgatcttcct	240
gacgcccata	ctgtcgctgt	cccctcaaac	tggcagatgc	acggttacga	cgccccatc	300
tacaccaacg	tgacatatcc	cattacggtc	aatccgcat	ttgttcccac	ggagaatccg	360
acgggttgtt	actcgctcac	attnaatgtt	gatgaaagct	ggctacagga	aggccagacg	420
cgttacggcc	aggacagtcg	tttgcgtgt	gaatttgacc	tgagcgcatt	tttacgcgcc	480
ggagaaaaacc	gcctcgccgt	gatggtgcgt	cgctggagtg	acggcagtta	tctggaaagat	540
caggatatgt	ggcggatgag	cggttacatttc	cgtgacgtct	cggtgtcgca	caaaccgacc	600
acacaaatca	gcgttaccc	tgttgcact	ctctttaatg	atgattttag	ccgcgcggta	660
ctggaggccag	aaatccatgt	gtacggcgag	ctgcgcgtat	agctgcgggt	gacggttct	720
ttgtggcagg	gtgaaacgc	ggtcgcgc	ggcaccgcgc	ctttcgccgg	tgaaattatc	780
gatgagcgtg	gcgttatgc	cgatcgctc	acactaggtc	tgaacgtcga	aaacccgaaa	840
ctgtggcg	ccgaaatccc	gaatatctat	cgtgcgggttgg	ttgaactgca	caccgcgcac	900
ggcacgcgt	ttgaagcaga	agcctgcgt	gtcggtttcc	gctgggtgcg	gattgaaaat	960
ggtctgtgc	tgctgaacgg	caagccgttgc	ctgattcgc	gctttaaccg	tcacgagcat	1020
catccctctgc	atggtcaggt	catggatgag	cagacgttgc	tgcaggatat	cctgtcta	1080
aagcagaaca	actttaacgc	cgtgcgtgt	tcgcattatc	cgaaccatcc	gctgtggta	1140
accctgtgc	accgcgtacgg	cctgtatgt	gtggatgaag	ccaatattga	aacccacggc	1200
atgggtccaa	tgaatcgct	gaccgtatgt	ccgcgcgtgt	taccggccat	gagcgaacga	1260
gtaacacgaa	ttgtacagcg	cgatcgtaat	cacccgagtg	tgtatcatctg	gtcgctgggg	1320
aatgagtcag	gccacggcgc	taatcacgac	gcactctatc	gctggattaa	atctgtcgat	1380
ccatcccgcc	cggtgcagta	tgaaggcgcc	ggagccgaca	cctccgcaac	cgatattatt	1440
tgcggatgt	acgcgcgcgt	ggatgaagac	cagcccttcc	cggtgtgcc	gaaatggtcc	1500
atcaaaaaat	ggcttcgct	gcctggagaa	atgcgcac	tgtatccttg	cgaatacgcc	1560
						1620

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<210> SEQ ID NO 66

<211> LENGTH: 1024

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 66

Met	Thr	Met	Ile	Thr	Asp	Ser	Leu	Ala	Val	Val	Leu	Gln	Arg	Arg	Asp
1				5					10				15		

Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro
20 25 30

Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr Asn Arg Pro
35 40 45

Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Gln Phe Val Trp Phe
50 55 60

Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu Glu Cys Asp Leu Pro
65 70 75 80

Asp Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr
85 90 95

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Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys Tyr Ser Leu Thr Phe
 115 120 125
 Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln Thr Arg Ile Ile Phe
 130 135 140
 Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys Asn Gly Arg Trp Val
 145 150 155 160
 Gly Tyr Gly Gln Asp Ser Arg Leu Leu Ser Glu Phe Asp Leu Ser Ala
 165 170 175
 Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val Met Val Leu Arg Trp
 180 185 190
 Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met Trp Arg Met Ser Gly
 195 200 205
 Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro Thr Thr Gln Ile Ser
 210 215 220
 Asp Phe His Val Ala Thr Leu Phe Asn Asp Asp Phe Ser Arg Ala Val
 225 230 235 240
 Leu Glu Ala Glu Val Gln Met Tyr Gly Glu Leu Arg Asp Glu Leu Arg
 245 250 255
 Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln Val Ala Ser Gly Thr
 260 265 270
 Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg Gly Tyr Ala Asp
 275 280 285
 Arg Val Thr Leu Gly Leu Asn Val Glu Asn Pro Lys Leu Trp Ser Ala
 290 295 300
 Glu Ile Pro Asn Ile Tyr Arg Ala Val Val Glu Leu His Thr Ala Asp
 305 310 315 320
 Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val Gly Phe Arg Glu Val
 325 330 335
 Arg Ile Glu Asn Gly Leu Leu Leu Asn Gly Lys Pro Leu Leu Ile
 340 345 350
 Arg Gly Val Asn Arg His Glu His His Pro Leu His Gly Gln Val Met
 355 360 365
 Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu Met Lys Gln Asn Asn
 370 375 380
 Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn His Pro Leu Trp Tyr
 385 390 395 400
 Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val Asp Glu Ala Asn Ile
 405 410 415
 Glu Thr His Gly Met Val Pro Met Asn Arg Leu Thr Asp Asp Pro Arg
 420 425 430
 Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg Met Val Gln Arg Asp
 435 440 445
 Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu Gly Asn Glu Ser Gly
 450 455 460
 His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp Ile Lys Ser Val Asp
 465 470 475 480
 Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Ala Asp Thr Ser Ala
 485 490 495
 Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val Asp Glu Asp Gln Pro
 500 505 510
 Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys Trp Leu Ser Leu Pro
 515 520 525

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Gly Glu Met Arg Pro Leu Ile Leu Cys Glu Tyr Ala His Ala Met Gly
530 535 540

Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln Ala Phe Arg Gln Tyr
545 550 555 560

Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Leu Val Asp Gln Ser Leu
565 570 575

Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser Ala Tyr Gly Gly Asp
580 585 590

Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys Met Asn Gly Leu Val
595 600 605

Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr Glu Ala Lys His Gln
610 615 620

Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Arg Thr Ile Glu Val Thr
625 630 635 640

Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu Leu Leu His Trp Thr
645 650 655

Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly Glu Val Pro Leu Asp
660 665 670

Val Ala Pro Gln Gly Lys Gln Val Ile Glu Leu Pro Glu Leu Pro Arg
675 680 685

Leu Glu Ser Thr Gly Gln Leu Trp Leu Thr Val His Val Val Gln Pro
690 695 700

Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile Ser Ala Trp Gln Gln
705 710 715 720

Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu Pro Ser Ala Pro His
725 730 735

Ala Ile Pro Gln Leu Thr Thr Ser Glu Thr Asp Phe Cys Ile Glu Leu
740 745 750

Asp Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser Gly Phe Leu Ser Gln
755 760 765

Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr Pro Leu Arg Asp Gln
770 775 780

Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly Val Ser Glu Ala Thr
785 790 795 800

Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp Lys Ala Ala Gly His
805 810 815

Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr Ala Asp Thr Leu Ala
820 825 830

Asp Ala Val Leu Ile Thr Thr Val His Ala Trp Gln His Gln Gly Lys
835 840 845

Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile Asp Gly Ser Gly Gln
850 855 860

Met Ala Ile Thr Val Asp Val Glu Val Ala Ser Asp Thr Pro His Pro
865 870 875 880

Ala Arg Ile Gly Leu Thr Cys Gln Leu Ala Gln Val Ala Glu Arg Val
885 890 895

Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr Pro Asp Arg Leu Thr
900 905 910

Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu Ser Asp Met Tyr Thr
915 920 925

Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg Cys Gly Thr Arg Glu
930 935 940

Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp Phe Gln Phe Asn Ile

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260

945	950	955	960
Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr Ser His His			
965	970	975	
Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile Asp Gly Phe His Met			
980	985	990	
Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser Val Ser Ala Glu Phe			
995	1000	1005	
Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu Val Trp Cys Gln			
1010	1015	1020	

Lys

<210> SEQ ID NO 67
<211> LENGTH: 1254
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 67

atgtactatt taaaaaacac aaacttttg atgttcgggtt tattctttt cttttacttt	60
tttatcatgg gagcctactt cccggttttc ccgatggc tacatgacat caaccatatac	120
agcaaaaatgt atacgggtat tattttgcc gctatttctc tgttctcgct attattccaa	180
ccgcgttttgc gtctgcttgc tgacaaactc gggctgcga aatacctgct gtggattatt	240
accggcatgt tagtcatgtt tgccgcgttc ttatttta ttttcgggccc actgttacaa	300
tacaacattt tagtaggatc gattgttggt ggtatattatc taggcgttttgc tttaacgcc	360
ggtgtgcgcag cagtagaggc atttatttgc aaagtcagcc gtcgcgttgc ttgcatttt	420
ggtcgcgcgc ggtatgttgg ctgtgttggc tggcgctgt gtgcctcgat tgccggcatc	480
atgttccaca tcaataatca gtttgcgttgc tggctgggc ctggctgtgc actcatctc	540
gccgttttac tcttttcgc caaaacggat gcgcctctt ctgcacggc tgccaatgc	600
gtagggtccca accattcgcc atttagcctt aagctggcac tggaaactgtt cagacagcc	660
aaactgtggc ttttgcact gtatgttatt ggcgttttgc gcacctacga tggttttgc	720
caacagtttgc ttaatttctt tacttcgttc ttgtctaccg gtgaacaggg tacgcgggta	780
tttgcgtac taacgacaat gggcgaatta cttaacgcct cgattatgtt ctttgcgc	840
ctgatcatta atcgcatcggttggaaaaac gcgcgtgc tggctggcac tattatgtct	900
gtacgtatata ttggcgtatc gttcgccacc tcagcgctgg aagtggttat tctgaaaacg	960
ctgcataatgt ttgaagtacc gttcgtgtgc gttggctgtc ttaaatatata taccagccag	1020
tttgaagtgc gttttcgc gacgatttat ctggctgtt tctgctttaa ttagcaactg	1080
gegatgatatt ttatgtctgt actggcgccaa aatatgtatg aaagcatcggttccaggc	1140
gettatctgg tgctgggtct ggtggcgctg gggttccatc taattccgt gttcacgtt	1200
agcggcccccg gccccgttttc cctgtgtgcgt cgtaagggtga atgaagtgc ttaa	1254

<210> SEQ ID NO 68
<211> LENGTH: 417
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 68

Met Tyr Tyr Leu Lys Asn Thr Asn Phe Trp Met Phe Gly Leu Phe Phe			
1	5	10	15
Phe Phe Tyr Phe Phe Ile Met Gly Ala Tyr Phe Pro Phe Phe Pro Ile			
20	25	30	

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Trp Leu His Asp Ile Asn His Ile Ser Lys Ser Asp Thr Gly Ile Ile
 35 40 45
 Phe Ala Ala Ile Ser Leu Phe Ser Leu Leu Phe Gln Pro Leu Phe Gly
 50 55 60
 Leu Leu Ser Asp Lys Leu Gly Leu Arg Lys Tyr Leu Leu Trp Ile Ile
 65 70 75 80
 Thr Gly Met Leu Val Met Phe Ala Pro Phe Phe Ile Phe Ile Phe Gly
 85 90 95
 Pro Leu Leu Gln Tyr Asn Ile Leu Val Gly Ser Ile Val Gly Gly Ile
 100 105 110
 Tyr Leu Gly Phe Cys Phe Asn Ala Gly Ala Pro Ala Val Glu Ala Phe
 115 120 125
 Ile Glu Lys Val Ser Arg Arg Ser Asn Phe Glu Phe Gly Arg Ala Arg
 130 135 140
 Met Phe Gly Cys Val Gly Trp Ala Leu Cys Ala Ser Ile Val Gly Ile
 145 150 155 160
 Met Phe Thr Ile Asn Asn Gln Phe Val Phe Trp Leu Gly Ser Gly Cys
 165 170 175
 Ala Leu Ile Leu Ala Val Leu Leu Phe Phe Ala Lys Thr Asp Ala Pro
 180 185 190
 Ser Ser Ala Thr Val Ala Asn Ala Val Gly Ala Asn His Ser Ala Phe
 195 200 205
 Ser Leu Lys Leu Ala Leu Glu Leu Phe Arg Gln Pro Lys Leu Trp Phe
 210 215 220
 Leu Ser Leu Tyr Val Ile Gly Val Ser Cys Thr Tyr Asp Val Phe Asp
 225 230 235 240
 Gln Gln Phe Ala Asn Phe Phe Thr Ser Phe Phe Ala Thr Gly Glu Gln
 245 250 255
 Gly Thr Arg Val Phe Gly Tyr Val Thr Thr Met Gly Glu Leu Leu Asn
 260 265 270
 Ala Ser Ile Met Phe Phe Ala Pro Leu Ile Ile Asn Arg Ile Gly Gly
 275 280 285
 Lys Asn Ala Leu Leu Leu Ala Gly Thr Ile Met Ser Val Arg Ile Ile
 290 295 300
 Gly Ser Ser Phe Ala Thr Ser Ala Leu Glu Val Val Ile Leu Lys Thr
 305 310 315 320
 Leu His Met Phe Glu Val Pro Phe Leu Leu Val Gly Cys Phe Lys Tyr
 325 330 335
 Ile Thr Ser Gln Phe Glu Val Arg Phe Ser Ala Thr Ile Tyr Leu Val
 340 345 350
 Cys Phe Cys Phe Phe Lys Gln Leu Ala Met Ile Phe Met Ser Val Leu
 355 360 365
 Ala Gly Asn Met Tyr Glu Ser Ile Gly Phe Gln Gly Ala Tyr Leu Val
 370 375 380
 Leu Gly Leu Val Ala Leu Gly Phe Thr Leu Ile Ser Val Phe Thr Leu
 385 390 395 400
 Ser Gly Pro Gly Pro Leu Ser Leu Leu Arg Arg Gln Val Asn Glu Val
 405 410 415

Ala

<210> SEQ ID NO 69
 <211> LENGTH: 1254
 <212> TYPE: DNA

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<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 69

atgtactatt	taaaaaacac	aaacttttgg	atgttcggtt	tattctttt	cttttactt	60
tttatcatgg	gaggctactt	cccggttttc	ccgatttggc	tacatgacat	caaccatatc	120
agcaaaaatgt	atacgggtat	tatTTTgt	gttatTTCTC	tgttctcgct	attattcaa	180
ccgctgtttg	gtctgctttc	tgacaactc	gggctgegca	aatacctgct	gtggattatt	240
accggcatgt	tagtcatgtt	tgccgcgttc	tttattttta	tcttcgggcc	actgttacaa	300
tacaacattt	tagtaggatc	gattgttgg	ggtatTTATC	ttggctttt	ttttaacgcc	360
ggtgtcgcccg	cagtagaggc	atttatcgag	aaagtcaGCC	gtcgcaGtaa	tttcgaattt	420
ggtgtcgccgc	ggatgtttgg	ctgtgttggc	tgggcgctgt	gtgcctcgat	tgtcgccatc	480
atgttcacca	tcaataatca	gttcgtttc	tggctgggtt	ctggctgtgc	actcatcctc	540
gcattttac	tcttttcgc	caaaacggat	gegcctctt	ccggcacgg	tgccaatgcg	600
gttaggtgc	accattccgc	atTTAGCCTT	aaactggcgc	tggAAACTGTT	cagacagcca	660
aaactgttgt	ttttgtcact	gtatgttatt	ggcgTTTCT	gcacctacga	tgttttgac	720
caacagtttgc	ctaatttctt	tacttcttc	tttgccaccc	gtgaacacagg	tacgcgggta	780
tttggctacg	taacgacaat	gggcgaatta	cttaacgcct	caattatgtt	ctttgcgc	840
ctgatcatta	atcgcatcg	tggaaaaat	gcccgtgc	tggctggcac	tattatgtct	900
gtacgttata	ttggctcatc	gttgcacc	tcagcgctgg	aagtggttat	tctgaaaacg	960
ctgcataatgt	ttgaagtacc	gttcctgctg	gtgggctgct	ttaaatatat	taccagccag	1020
tttgaagtgc	gttttcagec	gacgatttat	ctggctgttt	tctgcttctt	taagcaactg	1080
gcgatgattt	ttatgtctgt	actagcgggt	aatatgtatg	aaagcatcg	tttccagggc	1140
gcttatctgg	tgctgggtct	ggtggcgctg	ggcttcacct	taatttccgt	gttacgcctt	1200
agcggccccg	gcccgtttc	tctactgcgt	cgtcagggtga	atgaagtgc	ttaa	1254

<210> SEQ_ID NO 70

<211> LENGTH: 417

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 70

Met	Tyr	Leu	Lys	Asn	Thr	Asn	Phe	Trp	Met	Phe	Gly	Leu	Phe	Phe	
1							5		10			15			
Phe	Phe	Tyr	Phe	Phe	Ile	Met	Gly	Ala	Tyr	Phe	Pro	Phe	Phe	Pro	Ile
							20		25			30			
Trp	Leu	His	Asp	Ile	Asn	His	Ile	Ser	Lys	Ser	Asp	Thr	Gly	Ile	Ile
							35		40			45			
Phe	Ala	Ala	Ile	Ser	Leu	Phe	Ser	Leu	Leu	Phe	Gln	Pro	Leu	Phe	Gly
							50		55			60			
Leu	Leu	Ser	Asp	Lys	Leu	Gly	Leu	Arg	Lys	Tyr	Leu	Leu	Trp	Ile	Ile
							65		70			75			80
Thr	Gly	Met	Leu	Val	Met	Phe	Ala	Pro	Phe	Phe	Ile	Phe	Ile	Phe	Gly
							85		90			95			
Pro	Leu	Leu	Gln	Tyr	Asn	Ile	Leu	Val	Gly	Ser	Ile	Val	Gly	Gly	Ile
							100		105			110			
Tyr	Leu	Gly	Phe	Cys	Phe	Asn	Ala	Gly	Ala	Pro	Ala	Val	Glu	Ala	Phe
							115		120			125			
Ile	Glu	Lys	Val	Ser	Arg	Arg	Ser	Asn	Phe	Glu	Phe	Gly	Arg	Ala	Arg

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130	135	140
Met Phe Gly Cys Val Gly Trp Ala Leu Cys Ala Ser Ile Val Gly Ile		
145	150	155
160		
Met Phe Thr Ile Asn Asn Gln Phe Val Phe Trp Leu Gly Ser Gly Cys		
165	170	175
Ala Leu Ile Leu Ala Ile Leu Leu Phe Phe Ala Lys Thr Asp Ala Pro		
180	185	190
Ser Ser Ala Thr Val Ala Asn Ala Val Gly Ala Asn His Ser Ala Phe		
195	200	205
Ser Leu Lys Leu Ala Leu Glu Leu Phe Arg Gln Pro Lys Leu Trp Phe		
210	215	220
Leu Ser Leu Tyr Val Ile Gly Val Ser Cys Thr Tyr Asp Val Phe Asp		
225	230	235
240		
Gln Gln Phe Ala Asn Phe Phe Thr Ser Phe Phe Ala Thr Gly Glu Gln		
245	250	255
Gly Thr Arg Val Phe Gly Tyr Val Thr Thr Met Gly Glu Leu Leu Asn		
260	265	270
Ala Ser Ile Met Phe Phe Ala Pro Leu Ile Ile Asn Arg Ile Gly Gly		
275	280	285
Lys Asn Ala Leu Leu Leu Ala Gly Thr Ile Met Ser Val Arg Ile Ile		
290	295	300
Gly Ser Ser Phe Ala Thr Ser Ala Leu Glu Val Val Ile Leu Lys Thr		
305	310	315
320		
Leu His Met Phe Glu Val Pro Phe Leu Leu Val Gly Cys Phe Lys Tyr		
325	330	335
Ile Thr Ser Gln Phe Glu Val Arg Phe Ser Ala Thr Ile Tyr Leu Val		
340	345	350
Cys Phe Cys Phe Phe Lys Gln Leu Ala Met Ile Phe Met Ser Val Leu		
355	360	365
Ala Gly Asn Met Tyr Glu Ser Ile Gly Phe Gln Gly Ala Tyr Leu Val		
370	375	380
Leu Gly Leu Val Ala Leu Gly Phe Thr Leu Ile Ser Val Phe Thr Leu		
385	390	395
400		
Ser Gly Pro Gly Pro Leu Ser Leu Leu Arg Arg Gln Val Asn Glu Val		
405	410	415

Ala

<210> SEQ ID NO 71

<211> LENGTH: 122

<212> TYPE: DNA

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 71

gcgcaacgca attaatgtga gttagctcac tcattaggca ccccaggcgt tacactttat	60
gcttccggct cgtatgttgt gtggattgt gagcggataaa caatttcaca cagggaaacag	120
ct	122

<210> SEQ ID NO 72

<211> LENGTH: 122

<212> TYPE: DNA

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 72

gcgcaacgca attaatgtga gttagctcac tcattaggca ccccaggcgt tacactttat	60
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gcttccggct cgtatgttgt gtgaaattgt gacggataa caatttcaca caggaacag	120
ct	122

What is claimed is:

1. An isolated T7 RNA polymerase polypeptide comprising a variant of a polypeptide of SEQ ID NO: 2 wherein, the variant polypeptide is at least 95% identical to SEQ ID NO: 2 over the entire length thereof;

the variant polypeptide having at least two mutations in SEQ ID NO: 2 independently selected from two or more of the amino acid residues consisting of:

- (i) 84, Arg to His (R84H);
- (ii) 414, Ile to Val (V414I);
- (iii) 653, Asp to Gly (D653G);
- (iv) 698, Trp to Gly (W698G); and
- (v) 735, Val to Met (V735M);

the variant polypeptide has RNA polymerase activity; and the variant polypeptide has reduced rates of uninduced expression in a T7 expression system compared to a T7 RNA polymerase of SEQ ID NO: 2.

2. The isolated polypeptide of claim **1**, wherein the variant polypeptide has about the same or greater rates of induced expression in a T7 expression system compared to a T7 RNA polymerase of SEQ ID NO: 2.

3. The isolated polypeptide of claim **1**, wherein the variant polypeptide has lower rates of expression in a T7 expression system with non-inducing medium comprising 0.2% glucose media compared to a T7 RNA polymerase of SEQ ID NO: 2.

4. The isolated polypeptide of claim **1**, wherein the variant polypeptide has a temperature sensitive phenotype, wherein the temperature sensitive phenotype comprises non-expression of a target polynucleotide sequence under control of a T7 promoter when grown at 37° Celsius; and expression of a target polynucleotide under the control of a T7 promoter when grown at 30° Celsius.

5. The isolated polypeptide of claim **1**, wherein the variant polypeptide has a temperature non-sensitive phenotype, wherein the temperature non-sensitive phenotype comprises expression of a target polynucleotide under the control of a T7 promoter when grown at 37° Celsius.

6. The isolated polypeptide of claim **5**, wherein the temperature non-sensitive phenotype comprises expression of a target polynucleotide under the control of a T7 promoter when grown at 42° Celsius.

7. The isolated polypeptide of claim **1**, wherein the variant polypeptide

(a) has at least two mutations selected from the group consisting of R84H, V414I, D653G, W698G, and V735M and (i) comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24; SEQ ID NO: 26; SEQ ID NO: 28; SEQ ID NO: 30; and SEQ ID NO: 32; or (ii) is encoded by a polynucleic acid comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; and SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; SEQ ID NO: 29; or SEQ ID NO: 31;

(b) has at least three mutations selected from the group consisting of R84H, V414I, D653G, W698G, and V735M and (i) comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 34; SEQ ID NO: 36; SEQ ID NO: 38; SEQ ID NO: 40; and

SEQ ID NO: 42; SEQ ID NO: 44; SEQ ID NO: 46; SEQ ID NO: 48; SEQ ID NO: 50; and SEQ ID NO: 52; or (ii) is encoded by a polynucleic acid comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 33; SEQ ID NO: 35; SEQ ID NO: 37; SEQ ID NO: 39; and SEQ ID NO: 41; SEQ ID NO: 43; SEQ ID NO: 45; SEQ ID NO: 47; SEQ ID NO: 49; and SEQ ID NO: 51;

(c) has at least four mutations selected from the group consisting of R84H, V414I, D653G, W698G, and V735M and (i) comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 54; SEQ ID NO: 56; SEQ ID NO: 58; and SEQ ID NO: 60; or (ii) is encoded by a polynucleic acid comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 53; SEQ ID NO: 55; SEQ ID NO: 57; and SEQ ID NO: 59; or

(d) has at least five mutations of R84H, V414I, D653G, W698G, and V735M and (i) comprises an amino acid sequence of SEQ ID NO: 62 or (ii) is encoded by a polynucleic acid comprising a nucleic acid sequence SEQ ID NO: 61.

8. The isolated polypeptide of claim **1**, wherein the variant polypeptide (i) comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 32; SEQ ID NO: 50; and SEQ ID NO: 54; or (ii) is encoded by a polynucleic acid comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 31; SEQ ID NO: 49; and SEQ ID NO: 53.

9. The isolated polypeptide of claim **1**, wherein the variant polypeptide comprises the R84H mutation.

10. The isolated polypeptide of claim **1**, wherein the variant polypeptide comprises the D653G mutation.

11. The isolated polypeptide of claim **1**, wherein the variant polypeptide comprises the W698G mutation.

12. The isolated polypeptide of claim **1**, wherein the variant polypeptide comprises the V735M mutation.

13. The isolated polypeptide of claim **1**, encoded by a nucleic acid sequence having at least 95% identity to that of SEQ ID NO: 1 and at least one mutation selected from the group consisting of:

- (i) a mutation at base 251 of CGC to CAC;
- (ii) a mutation at base 1240 of ATC to GTC;
- (iii) a mutation at base 1958 of GAT to GGT;
- (iv) a mutation at base 2092 of TGG to GGG; and
- (v) a mutation at base 2203 of GTG to ATG.

14. An isolated polynucleic acid comprising a nucleic acid sequence having at least 95% identity to that of SEQ ID NO: 1 and at least one mutation selected from the group consisting of:

- (i) a mutation at base 251 of CGC to CAC;
 - (ii) a mutation at base 1240 of ATC to GTC;
 - (iii) a mutation at base 1958 of GAT to GGT;
 - (iv) a mutation at base 2092 of TGG to GGG; and
 - (v) a mutation at base 2203 of GTG to ATG;
- wherein the isolated polynucleic acid encodes a polypeptide having T7 RNA polymerase activity.

15. An expression system for producing a target polypeptide in a prokaryotic host cell, the expression system comprising an isolated nucleic acid construct, the isolated nucleic acid construct comprising:

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- (i) a first polynucleotide sequence (R) comprising a sequence encoding the T7 RNA polymerase polypeptide of claim 1;
 - (ii) a lac Z polynucleotide sequence (Z) encoding β-galactosidase;
 - (iii) a lac Y polynucleotide sequence (Y) encoding a β-galactoside permease; and
 - (iv) a wild-type lac control region (C) comprising a CAP binding site, a promoter, an operator, and a ribosome binding site;
- wherein (R) is located between (Z) and (Y), and ZRY is downstream of the wild-type lac control region (C); the promoter of (C) is a lac-inducible and catabolite-repressible promoter recognized by a prokaryotic host cell polymerase; and the polynucleotide sequence of (i), (ii), (iii), or (iv) is under the control of the lac-inducible and catabolite-repressible promoter.

16. The expression system of claim 15, wherein R further comprises a nucleotide sequence having at least 95% identity to that of SEQ ID NO: 1 and at least two mutations selected from the group consisting of (i) a mutation at base 1240 of ATC to GTC; (ii) a mutation at base 2092 of TGG to GGG; (iii) a mutation at base 2203 of GTG to ATG; (iv) a mutation at base 251 of CGC to CAC; and (v) a mutation at base 1958 of GAT to GGT; and the nucleotide sequence encodes the polypeptide of claim 1.

- 17.** The expression system of claim 15, wherein
- (a) the lac Z polynucleotide (Z) comprises
 - (i) a nucleotide sequence selected from group consisting of SEQ ID NO: 63 and SEQ ID NO: 65, or a variant having at least 95% identity thereof encoding a polypeptide having β-galactosidase activity;
 - (ii) a nucleotide sequence encoding a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 64 and SEQ ID NO: 66 and β-galactosidase activity, or a variant having at least 95% identity thereof and β-galactosidase activity; or
 - (iii) a lac Z polynucleotide from *E. coli* strain BL21;
 - (b) the lac Y polynucleotide (Y) comprises
 - (i) a nucleotide sequence selected from group consisting of SEQ ID NO: 67 and SEQ ID NO: 69, or a variant having at least 95% identity thereof encoding a polypeptide having β-galactoside permease activity;
 - (ii) a nucleotide sequence encoding a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 68 and SEQ ID NO: 70 and β-galactoside permease activity, or a variant having at least 95% identity thereof and having β-galactoside permease activity; or
 - (iii) a lac Y polynucleotide from *E. coli* strain BL21; or
 - (c) the wild-type lac control region (C) comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 71 and SEQ ID NO: 72, or a variant having at least 95% identity thereof having a functional CAP binding site, promoter, operator, and ribosome binding site.

18. The system of claim 15, further comprising a second polynucleotide sequence, the second polynucleotide sequence comprising

- a target promoter polynucleotide sequence recognized by the encoded T7 RNA polymerase of the isolated nucleic acid construct; and
- a target polynucleotide sequence encoding a target polypeptide;

wherein the target polynucleotide sequence is under the control of the target promoter polynucleotide sequence.

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19. The system of claim 15, further comprising a host cell, wherein the host cell comprises the isolated nucleic acid construct; and optionally, one or more of the following conditions:

- 5 (a) the host cell further comprises a polynucleotide encoding a colorimetric positive indicator of T7 RNA polymerase expression;
- (b) the host cell further comprises a polynucleotide encoding a DsRed.T3. colorimetric positive indicator of T7 RNA polymerase expression;
- (c) the host cell is an *E. coli* cell;
- (d) the host cell is an *E. coli* strain selected from the group consisting BL21, C2566, DH1, DH4I, DH5, DH5I, DH5IF, DH5IMCR, DH10B, DH10B/p3, DH11S, C600, HB101, JM101, JM105, JM109, JM110, K38, MG1655, RR1, Y1088, Y1089, CSH18, ER1451, and ER1647;
- (e) wherein the host cell is *E. coli* strain BL21; or
- (f) wherein the host cell is selected from the group consisting of *E. coli* strain WB456.7, *E. coli* strain WB466.15, *E. coli* strain WB478e, and *E. coli* strain WB477f.

20. A method for producing a target polypeptide in a host cell, the method comprising:

- (a) introducing into a host cell the expression system of claim 15;
- (b) introducing into the host cell a second polynucleotide sequence comprising
 - (i) a target polynucleotide sequence encoding a target polypeptide; and
 - (ii) a target promoter polynucleotide sequence recognized by the encoded T7 RNA polymerase of (R) of the expression system;

wherein the target polynucleotide sequence is under the control of the target promoter polynucleotide sequence;
- (c) incubating the host cell under conditions appropriate for expression of a T7 RNA polymerase encoded by the first polynucleotide sequence (R) and expression of the target polypeptide from the target polynucleotide sequence.

21. An isolated T7 RNA polymerase polypeptide comprising a variant of a polypeptide of SEQ ID NO: 2 wherein, the variant polypeptide is at least 95% identical to SEQ ID NO: 2 over the entire length thereof;

the variant polypeptide has a mutation in SEQ ID NO: 2 at amino acid residue 698, Trp to Gly (W698G); the variant polypeptide has at least one additional mutation in SEQ ID NO: 2 at amino acid residue positions selected from the group consisting of:

- (i) amino acid residue 84, Arg to His (R84H);
- (ii) amino acid residue 414, Ile to Val (V414I);
- (iii) amino acid residue 653, Asp to Gly (D653G); and
- (iv) amino acid residue 735, Val to Met (V735M);

the variant polypeptide has RNA polymerase activity; and the variant polypeptide has reduced rates of uninduced expression in a T7 expression system compared to a T7 RNA polymerase of SEQ ID NO: 2.

22. The isolated T7 RNA polymerase polypeptide of claim 21, wherein

- the variant polypeptide comprises mutations selected from the group consisting of:
- (i) amino acid residue 414, Ile to Val (V414I), amino acid residue 698, Trp to Gly (W698G), and amino acid residue 735, Val to Met (V735M);
 - (ii) amino acid residue 698, Trp to Gly (W698G) and amino acid residue 735, Val to Met (V735M); or

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(iii) amino acid residue 84, Arg to His (R84H), amino acid residue 414, Ile to Val (V414I), amino acid residue 653, Asp to Gly (D653G), and amino acid residue 698, Trp to Gly (W698G);

the variant polypeptide has RNA polymerase activity; and
the variant polypeptide has reduced rates of uninduced expression in a T7 expression system compared to a T7 RNA polymerase of SEQ ID NO: 2.

23. The isolated T7 RNA polymerase polypeptide of claim 21, wherein

the variant polypeptide comprises mutations selected from the group consisting of:

(i) amino acid residue 414, Ile to Val (V414I), amino acid residue 698, Trp to Gly (W698G), and amino acid residue 735, Val to Met (V735M); or

(ii) amino acid residue 698, Trp to Gly (W698G) and amino acid residue 735, Val to Met (V735M);

the variant polypeptide has RNA polymerase activity;
the variant polypeptide has reduced rates of uninduced expression in a T7 expression system compared to a T7 RNA polymerase of SEQ ID NO: 2; and the variant polypeptide has temperature sensitivity in a T7 expression system compared to a T7 RNA polymerase of SEQ ID NO: 2.

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